GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Minimum DB seq
Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
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Perfect score:
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2681
1 MFETEHHTLLPLLLL
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length: 2000000000
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1: /SIDS2/gcgdata/g
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA199, DAT:

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA100, DAT:

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000, DAT:

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1020.262 million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SIMMARTE

10	9	80	7	σ	ر. ت	4	ω	2	1	No.	1
816.5	866	946	946	978.5	978.5	978.5	978.5	978.5	2681	Score	
30.5	32.3	35.3	35.3	36.5	36.5	36.5	36.5	36.5	100.0	Match Length DB	,
486	512	444	444	492	491	472	472	472	513	Length I	
22	23	21	21	21	21	21	21	18	21		
AAU02839	ABB91571	AAG45023	AAG44572	AAG44570	AAG45021	AAG45022	AAG44571	AAW27153	AAB07921	ID	
Taxus cuspidata ox	Herbicidally activ	Arabidopsis thalia	A cytochrome P450	Description							

PT DR XX

Azpiroz R,

Choe S,

Feldmann KA;

(ARIZ-) ARIZONA BOARD OF REGENTS.

WPI; 2000-549142/50. N-PSDB; AAA59599.

New isolated dwf4 polynucleotide useful for altering the phenotype of plants, for diagnostic assays and in the production of antibodies -

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ć	7.4	43	42	41	40	39	38	37	36	35 .	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
. d	490	503	503	503	503	N3	534.5	546	547.5	553.5	558.5	558.5	564	564	568.5	569.5	571	583	585	588	592	596.5	597.5	598.5	603	606	606	653.5	712	712	712	726	726	726
	18.3	18.8	18.8	18.8		٠	19.9	20.4	20.4	20.6	20.8	20.8	21.0		21.2									22.3										27.1
407	433	492	492	492	492	388	503	481	489	498	512	483	500	484	500	493	501	484	507	509	496	497	485	430	469	479	471	468	465	462	461	465	462	461
13	27	23	22	19	19	21	22	21	21	22	22	22	22	22	22	22	22	22	22	22	22	22	22	21	21	21	21	21	21	21	21	21	21	21
PERMIT A TOO	AAG30050	AAE15325	AAB85155	AAW44159	AAW37733	AAG20785	AAU02828	AAG30049	AAG30048	AAU02838	AAU02834	AAU02827	AAU02826	AAU02821	AAU02824	AAU02836	AAU02823	AAU02822	AAU02830	AAU02832	AAU02837	AAU02829	AAU02835	AAG20784	AAG23014	AAG23012	AAG23013	AAG20783	AAG11834	AAG11835	AAG11836	AAG46491	AAG46489	AAG46490
CYCOCIILOINE FAJORAL		Zebrafish P450RAI	Zebrafish cytochro	Zebrafish retinoid	Cytochrome zP450RA		α.		dopsis thal	cuspidata		cuspidata	a					-						Arabidopsis thalia										

ALIGNMENTS

RESULT 1

AAB07921	7921
ΧIJ	AAB07921 standard; Protein; 513 AA.
AC	AAB07921;
××	
DT	14-NOV-2000 (first entry)
××	
DE	A cytochrome P450 enzyme designated DWF4.
XX	
KΨ	DWF4; cytochrome P450 enzyme; brassinosteroid; 22alpha-hydroxylation;
×Ψ	plant phenotype; cell elongation.
××	
20	Arabidopsis sp.
××	
ΡN	WO200047715-A2.
XX	
PD	17-AUG-2000.
××	
PF	11-FEB-2000; 2000WO-US03820.
×	
PR	11-FEB-1999; 99US-0119657.
PR	11-FEB-1999; 99US-0119658.
4	

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ARESULT 2
AAW27153
ID AW2
XX AAW2
AC AAW2
XX 11 -A
DT 11 -A
DT 12 -A
DE Arab
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Best Local
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22alpha-hydroxylation steps in brassinosteroid biosynthesis. The DWF4
polynucleotide is used for altering the phenotype of a plant. DWF4
polynucleotide is deferred to reduction in the length of different organs, and this size reduction is attributable to a defect in cell elongation. The DWF4 polynucleotides and polypeptides can be used in diagnostic assays and to generate antibodies, which can be used to produce
             Arabidopsis thaliana
                                                       Cytochrome P450-type hydroxylase; identification; brassinosteroid; brassinosteroid inhibitor; modified plant; recombinant production;
                                                                                                                                  14-APR-1998
                                                                                                                                                                                         AAW27153 standard;
                                                                                                 Arabidopsis thaliana cytochrome P450-type hydroxylase.
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                                                                                                                                                                                                                                                                                                                                         QPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLV
                                                                                                                                                                                                                                                                                                                                                                                                   YKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKWSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEA
                                                                                                                                                                                                                                                                                                                                                                                  YKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYD
                                                                                                                                                                                                                                                                                                                                                                                                                                         ILDLILSLLFAGHETSSVAIALAIFFLOACPKAVEELREEHLEIARAKKELGESELNWDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKFTFNLMAKHIMSMDPGEEETEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILK
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                                                                                                                                                                                                                                                                 LKFNWELAEDDQPFAFPFVDFPNGLPIRVSRIL
                                                                                                                                                                                                                                                                                                                        QPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 100.
13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          513 AA;
                                                                                                                             (first entry)
                                                                                                                                                                                          Protein; 472
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Pred. No. 1.3e-228;
D; Mismatches 0;
                                                                                                                                                                                                                                                                                            513
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Matches 210;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is Arabidopsis thaliana cytochrome P450-type hydroxylase. The hydroxylase can be used to identify brassinosteroids or brassinosteroid inhibitors, useful to produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Pages 44-46; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated plant cytochrome P450-type hydroxylase gene - used to identify substances acting as brassino-steroid(s) or brassinosteroid inhibitors for the production of modified plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09735986-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  compounds, e.g.
                                                                                                                                            NETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMSMDPGEEETEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILKFIERKMEERKL
                                                                                                                                                                                                                                                                                   GHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDYKKMDFTQCVI
                                                                                                                                                                                                                                                                                                                                                                                                  DIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSNLSTEQILDLILSLLFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LHKRMHSLTMSFANSSIIKDHLMLDIDRLVRFNLDSWSSRVLL--MEEAKKITFELTVKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARYGSVFMTHLFGEPTIFSADPETNRFVLQNEGKLFECSYPASICNLLGKHSLLLMKGS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLLLSSIAAGFL---LLLRRTRYRRMGLPPGSLGLPLIGETFQLIGAYKTENPEPFIDER 63
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                                                     QQNNGASSSGSGSFSTWGNN-YMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAED
                                                                                                           NETLRVANIIGGVFRRAMTDVEIKGYKIPKGWKVFSSFRAVHLDPNHFKDARTFNPWRWQ
                                                                                                                                                                                                                             GYETTSTIMTLAVKFLTETPLALAQLKEEHEKIRAMKSD--SYSLEWSDYKSMPFTQCVV
                                                                                                                                                                                                                                                                                                                                               VVVMKRREEEEEGAE - - - - - - - - - - - - RKKDMLAALLAADDGFSDEEIVDFLVALLVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LMSFDPG-EWSESLRKEYLLVIEGFFSLPLPLFSTTYRKAIQAR-----RKVAEALT
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SNSVTTGPSNVFTPFGGGPRLCPGYELARVALSVFLHRLVTGFSWVPAEQ
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RESULT 3
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09-MAR-1999;
23-MAR-1999;
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netic mapping; gene expression control; promoter;
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9908-014814.
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311 232 251

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Query Match 36.5%;
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Matches 210; Conservative 7
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3-0161989

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S-0149722.
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3-0151080.
3-0151303.
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S-0150566.
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                                                                            Score 978.5; DB 21;
Pred. No. 6.6e-78;
9; Mismatches 171;
                                                                                           DB 21;
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                                                                                                                                                                                                                                              Arabidopsis thaliana.
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99US-0128714
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pathway;
promoter;

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11-MAY-1999; 14-MAY-1999; 14-MAY-1999; 14-MAY-1999; 11-MAY-1999; 11-MAY-1999; 12-MAY-1999; 22-MAY-1999; 23-MAY-1999; 24-MAY-1999; 25-MAY-1999; 26-MAY-1999; 27-MAY-1999; 27-MAY-1999; 28-MAY-1999; 28-MAY-1999; 28-MAY-1999; 28-JUN-1999; 28-JU
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   06-SEP-2000.
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                                                                         Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
                                                                                                                                                                    AAG45021 standard;
                        EP1033405-A2
                                          Arabidopsis thaliana
                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 56468.
                                                                                                                              18-OCT-2000
                                                                                                                                                                                                                          447
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LKRMHSLTMSFANSSIIKDHLMLDIDRLVRFNLDSWSSRVLL--MEEAKKITFELTVKQ
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                                                                                                                                                                                                                                                                                                                                                                                                       IMSMDPGEEETEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILKFIERKMEERKL
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al Similarity 41.9%;
210; Conservative
                                                                                                                            (first entry)
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990S-0161359.
990S-0161361.
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990S-0161920.
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990S-0161993.
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99US-0160989.
99US-0161404.
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Pred. No. 6.6e-78;
9; Mismatches 171;
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promoter;
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8-SEP-1999;
9-SEP-1999;
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                                                      LHKRMHSLTMSFANSSIIKDHLMLDIDRLVRFNLDSWSSRVLL--MEEAKKITFELTVKQ
                                                                                                                                                                                                        LLLLPSLLSLLLELILLKRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDFMQQH
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990S-0161359.
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                                                                                                                                                                                                                           Score 978.5; DR
Pred. No. 7e-78;
9; Mismatches 1
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07-OCT-1999;
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     VSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLVGD 131
                                                       LLLLSSIAAGFL---LLRRTRYRRMGLPPGSLGLPLIGETFQLIGAYKTENPEPFIDER
                                                                            LLLLPSLLSLLLFLILLKRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDFMQQH
                                                                                                                             Conservative
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41.9%; Pred. No. 7e-78;
tive 79; Mismatches 171;
Indels
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Pred. No. 4.6e-
77; Mismatches
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No. 4.6e-75;
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                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequence from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tietjen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-AUG-2001; 2001WO-EP09892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herbicidal; plant; agriculture; herbicide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herbicidally
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                                                                                                                                                                                                                                                                          12 LLLLPSLLSLLLFLIL-----LKRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGD
                                                                                                                                                                                                                                                                                                                     Local
2002-269010/31
                                                             NLPGTAYHKALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQR
                                                                                         LQTLSNFKDGEVVLLQDICRKVAIHLMVNQLLGVS-SESEVDEMSQLFSDFVDGCLSVPI
                                                                                                                  LFVLDSWQQNSIFSAQDEAKKFTFNLMAKHIMSMDPGEEETEQLKKEYVTFMKGVVSAPL
                                                                                                                                             QNEGKLFQSSYPKSFRDLVGKDGVITVHGDQQRRLHSIASSMMRHDQLKTHFLEVIPVVM
                                                                                                                                                                     QNEGRLFECSYPRSIGGILGKWSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHT
                                                                                                                                                                                                FVEKQIKKFVSLLCSVLLLILKRPDNSGFNEIRYGRIFSCSLFGKWAVVSADPDFNRFIM
                                                                                                                                                                                                                                                   LLSVSSSTTFLAFIIIFLLAGIARRKRRAPHRLPPGSRGWPLIGDTFAWLNAVAGSHPSS
                                       DLPGFTYNKAMKARKEIIRKINKTIEKRLQNKAASD-----
                                                                                                                                                                                                                                                                                                       181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                    as herbicides.
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                                                                                                                                                                                                                                                                                                    Score 866; DB 23;
Pred. No. 6.8e-68;
5; Mismatches 173;
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                                                                                                                                                                                                                                                                                                      Indels
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LFICVILLLLRRSNDRQGNGSANKPKLPPGSAGLPFIGETIRFLRDAKSPGRRKFFDEHE

LSLLLFLILLKRRNRK-----TRENLPPGKSGWPFLGETIGYLKPYTATTLGDFMQQHV 72

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Matches Query Match

hes 176;

Similarity

30.5%;

Score 816.5; DB 2 Pred. No. 1.5e-63;

DB 22; 184;

Conservative

97;

Mismatches

Indels Length 486;

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Gaps

8

79

Sequence

486

AA;

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RESULT 10
AAU02839
                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acid and amino acid sequences, isolated from genus, useful for the synthetic production of Taxol and retaxolds, intermediates within the Taxol biosynthetic pathw
transgenic organism. The oxygenase nucleic acids and amino acids are useful for isolating the polynucleotide and polypeptide sequences corresponding to full-length oxygenases.
                                                                          can be used to make transgenic organisms that either produce the oxygenases for subsequent in vitro use, or produce the oxygenases in oxygenases to alter the level of Taxol and taxold production within the
                                                                                                                                                           The sequence represents a Taxus cuspidata oxygenase, encoded by a DNA of the invention. The sequences isolated from the Taxus genus, and the respective oxygenases are useful for the synthetic production of Taxol and related taxolds, as well as intermediates within the Taxol biosynthetic pathway, and other taxold derivatives. The sequences also
                                                                                                                                                                                                                                                                                                                           Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                          taxoids, intermediates within other taxoid derivatives -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GWKVLPVISAVHLDNSRYDQPNLFNPWRW-----QQQNNGASSSGSGSFSTWGNNYMPFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-355489/37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTRFCPGAELARLQIALFLHYFITTYKWTQLKEDRISFFPSARLVNGFKIQLNR
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                                                                                                                                                                                                                                                                                                                        Page 139-141; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                          Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG46490;
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         termination
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91; Mismatches 181;
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              pathway;
promoter;
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                                                                                   STEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESEL: |: | | | | |::: | | | |::: | | | |::: | | | | |::: | | | | |::: | | | | |::: | | | | |::: | | | | | |::: | | | | | |::: | | | | | |::: | | | | | |::: | | | | | |::: | | | | | |::: | | | | | | |::: | | | | | |::: | | | | |::: | | | | |::: | | | | |::: | | | | |::: | | | |::: | | | |::: | |::: | |::: | |::: | |::: | |:: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: | |::: |:: | |::: | |::: | |::: |:: | |::: |:: | |::: |:: | |::: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |::
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990S-0151066
990S-0161066
                          Score 726; DB Pred. No. 1.5e-91; Mismatches
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Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
                             Arabidopsis thaliana protein fragment SEQ ID
                                                                  AAG11835;
                                                                                    AAG11835 standard; Protein; 462
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Search completed: March 30, Job time: 69 secs 2003, 12:04:18 QΥ 밁

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RESULT 2
US-08-622-166A-4
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                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                        REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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                          TELEFAX: 1/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAKKFTFNLMAKH 191
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                                                                                                                                                                                                                                                                                                                                                    22040-0747
                                                                                                                                                                                                                                                                                                                                                                                                     T: P.O. Box 7
Falls Church
                                                                                                                                                                                                                                                                                                                                                                 Virginia
Y: USA
                                                                                                                                                SVENSSON, LEONARD R.
     CHARACTERISTICS
                                                      (703)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTMANN, THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MATHUR, JAIDEEP
SZEKERES, MIKLOS
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                                                                                                                                                                                                                                                                                                                                                                                                                       Birch, Ste
                                                                             (703)
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                                                        205-8050
                                                                         205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEIC ACID MOLECULES ENCODING CYTOCHROME P450-TYPE PROTEINS INVOLVED IN THE BRASSING
                                                                                                                                                                                                                                                                                                                                                                                                                                        Stewart, Kolasch & Birch,
                                                                                                                                                                                                                        US/08/622,166A
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                                                                                                                                                                                                                                                         (EPO)
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US-08-724-466B-2
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Best Local S
Matches 210
                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08724466B Patent No. 6063606 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: prot
                               FILING DATE: October 1, 1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Ca
                                                                                                                                                                                                                                                                                                          APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Beckett, Barbara R., Jones, Glenvill TITLE OF INVENTION: Retinoid Metabolizing Prote NUMBER OF SEQUENCES: 30
                                                                                      CURRENT APPLICATION DATA:
                                                                                                 COMPUTER: COMPAQ, IBM PC
OPERATING SYSTEM: MS-DOS SOFTWARE: WORD PEDEFORM
TREET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252 DIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSNLSTEQILDLILSLLFA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 LMSFDPG-EWSESLRKEYLLVIEGFFSLPLPLFSTTYRKAIQAR------RKVAEALT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 LHKRMHSLTMSFANSSIIKDHLMLDIDRLVRFNLDSWSSRVLL--MEEAKKITFELTVKQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 472 amino acids
                                                                                                                                                                                                     ZIP: M5L 1A9
COUNTRY: Canada
                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 LLLLPSLLSLLLFLTLLKRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDFMQQH 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 VSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLVGD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQNNGASSSGSGSFSTWGNN-YMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAED 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NETLRVANIIGGVFRRAMTDVEIKGYKIPKGWKVFSSFRAVHLDPNHFKDARTFNPWRWQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NETLRIGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQ 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GYETTSTIMTLAVKFLTETPLALAQLKEEHEKIRAMKSD--SYSLEWSDYKSMPFTQCVV 336
                                                                                                                                                                                                                                   Toronto
                                                                                                                                                                                                                                                        Box 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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June 21,
                                                                                                                                                                                                                                                         Commerce
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41.9%; Pred. No. 5e
                                                                                                                                                                                                                                                                       Cassels & Graydon
                                                                       US/08/724,466B
 08/667,546
1, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79; Mismatches 171;
                                                                                                                            compatible 5.1
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                                                                                                                                                               1.4 Mb
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5e-89;
                                                                                                                                                                                                                                                                                                                                                Glenville
                                                                                                                                                               storage
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US-08-724-466B-2
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                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08882164D Patent No. 6306624 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (416) 863-2653 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
                                                                                                                                                                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                          APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: Hunt, John C.
       COMPUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 ILGKWSMLVLVGDMHRD-----MRSISLNFLSHARLRTILLKDVERHTLFVLDSW-QQNS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                COUNTRY:
                                                                              STATE:
                                                                                                                       STREET:
                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 YTLMVTFLCTIVLPVLLFLAAVKLWEMLMIRRVDPNCRSPLPPGTMGLPFIGETLQLI--
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Local Similarity 27.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKE 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAKLEMAVFIHHLVLKFNWELAEDDQ-----PFAFPFVDFP 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSE 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LG----ESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVL 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALQSRATILKFIERKMEERKLDIKEEDQEEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWV 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IFSAQDEAKKFTFNLMAKHIMSMDPGEEET -- EQLKKEYVTFMKGVVSAPLNLPGTAYHK 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YTATTLGDFMQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FAKVLLKIFLVELTQHCNWILSNGPPTMKTGPTIYPVDNLP 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGMYTPGKGLSMELLDQLKYTGCVIKETLRINPPVPGGFRVALKTFELNGYQIPKGWNVI 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----PFSLQAMKEAATELLFGGHETTASTATSLVMFLGLNTEVVQKVREE----VQEKVE 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLRAR----IENSRIEENIRKKIQDDDNENEQKYKDALQLL----IENSRRSDE----
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                             RY: Canada
                                                                                                 Toronto
  READABLE FORM:
                                                                         Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               492 amino acids
                                                                                                                       Box 25,
                                                                                                                                             Blake, Cassels & Graydon
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                                                                                                                     Commerce Court West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95; Mismatches 216; Indels
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                     RESULT 5
US-08-802-164D-32
; Sequence 32, Application US/08882164D
; Patent No. 6306624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (416) 863-2653 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10508444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: October 1, ATTORNEY/AGENT INFORMATION: NAME: Hunt, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/882,164D FILING DATE: June 25, 1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 CVLVYPEMKKLMFRIAMRILLGFEPEQIKTDEQELVEAFEEMIKNLFSLPIDVPFSGLYR
                                                                                                                                                                                                                                                                392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 ALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 ILGKWSMLVLVGDMHRD-----MRSISLNFLSHARLRTILLKDVERHTLFVLDSW-QQNS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette, 3 1/2 inch, COMPUTER: COMPAQ, IBM PC compatible OPERATING SYSTEM: MS-DOS 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 18.8%;
Local Similarity 27.6%;
nes 144; Conservative 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 ----LQRRKFLRMKRQKYGCIYKTHLFGNPTVRVMGADNVRQILLGEHKLVSVQWPASVRT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 YTATTLGDFMQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 36,424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 YTLMVTFLCTIVLPVLLFLAAVKLWEMIMIRRVDPNCRSPLPPGTMGLPFIGETLQLI-- 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 HTLLPLLLLPSLLSLLLFL------ILLKRRNRKTRFNLPPGKSGWPFLGETIGYLKP 58
                                                                                                                                                                                                             LAKLEMAVFIHHLVLKFNWELAEDDQ-----PFAFPFVDFP 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                ----PFSLQAMKEAATELLFGGHETTASTATSLVMFLGLNTEVVQKVREE----VQEKVE
                                                                                                                                                                                                                                                                                                                                                                                   LG----ESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVL 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLRAR----IENSRRSDE----
                                                                                                                                                              FAKVLLKIFLVELTQHCNWILSNGPPTMKTGPTIXPVDNLP 483
                                                                                                                                                                                                                                                           YSICDTHDVADVFPNKEEFQPERFM-----SKGLEDGSRF--NYIPFGGGSRMCVGKE 442
                                                                                                                                                                                                                                                                                                       PVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSE
                                                                                                                                                                                                                                                                                                                                                   MGMYTPGKGLSMELLDQLKYTGCVIKETLRINPPVPGGFRVALKTFELNGYQIPKGWNVI 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IFSAQDEAKKETFNLMAKHIMSMDPGEEET--EQLKKEYVTFMKGVVSAPLNLPGTAYHK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILGSDTLSNVHGVQHKNKKKAIMRAFSRDALEH-----YIPVIQQEVKSAIQEWLQKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      492 amino acids
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Pred. No. 1.5e-41;
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US-08-882-164D-32
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Best Local Sim
Matches 148;
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REGISTRATION NUMBER: 5076'
REFERENCE/DOCKET NUMBER: 5076'
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (416) 863-269
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: June 25, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: 08/667,546
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 GILGKWSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQ--NSIFS 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: COMPAQ, IBM PC compatible OPERATING SYSTEM: MS-DOS 5.1 SOFTWARE: WORD PERFECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 LPLLLLPSL----LSLLLFLILLK------RRNRKTRFNLPPGKSGWPFLGETIGYLK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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PVISAVHLDNSRYDQPNLENPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSE
                                                                 LCKSNQDNKLDMETLEQLKYIGCVIKETLRLNPPVPGGFRVALKTFELNGYQIPKGWNVI 395
                                                                                             AKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVL
                                                                                                                                                                                                                                               VKARNLIHARIEENIRAKIRRLQATEPDGGCKDALQLLIEHSWE-----RGERLDMQ-
                                                                                                                                                                                                                                                                                                                                        VYPEVKRLMFRIAMRILLGCEPGPAGGGEDEQQLVEAFEEMTRNLFSLPIDVPFSGLYRG
                                                                                                                                                                                                                                                                                                                                                                                  AQDEAKKFTFNLMAKHIMSMDPGE----EETEQLKKEYVTFMKGVVSAPLNLPGTAYHKA 231
                                                                                                                                                                                                                                                                                                                                                                                                                              TILGAGCLSNLHDSSHKQRKKVIMQAFSREALQCYVLV-IAEEVSSCLEQWLSCGERGLL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYTATTLGDFMQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPALLASALCTFVLPLLLFLAALKLWDLYCVSSRDRSCALPLPPGTMGFPFFGETL----
                                                                                                                                                       ---ALKQS--STE------LLFGGHETTASAATSLITYLGLYPHVLQKVREEIKSKGL
                                                                                                                                                                                                   LGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIAR
                                                                                                                                                                                                                                                                                         LQSRATILKFIERKMEE--RKLDIKEED---QEEEEVKTEDEAEMSKSDHVRKQRTDDDL 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -QMVLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGEHRLVSVHWPASVR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          i: 497 amino acids amino acid
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Y: Canada
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.2%; Score 461; DB 4; Length 497; 28.4%; Pred. No. 2.4e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/882,164D
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                    466
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: June 21, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 5076
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskete, 3 1/2 inch, 1
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                      174 GLLVYPEVKRLMFRIAMRILLGCEPQLAGDGDSE-QQLVEAFEEMTRNLFSLPIDVPFSG
                                                                                                                                                                                                       118
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                                                                                                                                                                                                                                           118 GILGKWSMLVLVGDMHRDMRSISLNFLSHARLR---TILLKDVERHTLFVLDSWQQ--NS 172
                                                                                                                                                                                                                                                                                    59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                          58
                                                                                                                                                                                                                                                                                                                                                                                                     10 LPLLLLPSL----LSLLLFLILLK------RRNRKTRFNLPPGKSGWPFLGETIGYLK 57
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                                                                                                                                                                                                   TILGSGCLSNLHDSSHKQRKKVIMRAFSREALECYVPVITEEVGSS----LEQWLSCGER 173
DDDLLGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHL
                                     LYRGMKARNLIHARIEQNIRAKICGLRASEAGQGCKDALQLLIEHSWE-----RGERL
                                                                            YHKALQSRATILKFIERKMEERKLDIKEED-----QEEEEVKTEDEAEMSKSDHVRKQRT 282
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                                                                                                                                                            IFSAQDEAKKETENLMAKHIMSMDP-----GEEETEQLKKEYVTEMKGVVSAPLNLPGTA 227
                                                                                                                                                                                                                                                                                  -QMVLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGDDRLVSVHWPASVR 117
                                                                                                                                                                                                                                                                                                                        PYTATTLGDFMQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIG 117
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'RY: Canada
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US-08-882-164D-4
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                                                                                                                                                                                                                                                                                                                                 TELEFAX: (416) 863-26
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/882,164D FILING DATE: June 25, 1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA:
118 GILGKWSMLVLVGDMHRDMRSISLNFLSHARLR---TILLKDVERHTLFVLDSWQQ--NS
                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein
                                                                         58
                                                                                                                            10 LPLLLLPSL----LSLLLFLILLK-----RRNRKTRENLPPGKSGWPFLGETIGYLK 57
                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
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                                                             PYTATTLGDFMQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIG 117
                                                                                               LPALLASALCTFVLPLLLFLAAIKLWDLYCVSGRDRSCALPLPPGTMGFPFFGETL----
                              -QMVLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGDDRLVSVHWPASVR 117
                                                                                                                                                                    142;
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116) 863-2653
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June 21, 1990
NUMBER: 08/724,466
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                                                                                                                                                                              Score 439; DB 4; Length 497; Pred. No. 3.7e-35;
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SEQ ID NO 405
LENGTH: 529
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                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 405, Appl
Patent No. 6410718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US (
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US (
PRIOR FILING DATE: 1996-09-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 11000.1003c4U
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1998-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Materials and Methods TITLE OF INVENTION: Modification of Plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
163 VRDEVDIMVRIVAGSEGTAVNIGELVFELTRDIIYRAAFGTSSTEG-QDEFISILQEFSK 221
                                            176 AQDEAK ----
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                                                                                               GGILGKWSMLVLVGDMHRDMRSIS-LNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFS 175
                                                                                                                              GLASLAKKYGGIFHLRMGFLHMVAVSSPDVARQVLQVHDGIFSNRPATIAISYLTYDRAD 130
                                                                                                                                                             HVS----KYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFE------CSYPRSI 116
                                                                    ----MAFAHYGPFWRQMRKLCVMKLFSRKR-----
                                                                                                                                                                                                  PMTLLLSVVPLLLFLGLVARLRRKPPF--PPGPRGLPVIGNML
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21.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              us 08/713,000
                                                                                                                                                                                                                                                                  104;
                                  -KFTFNLMAKHIMSMDPGEEETEQLKKEYVTFMK----
                                                                                                                                                                                                                                                              Score 302.5; DB 4
Pred. No. 1.7e-21;
4; Mismatches 204
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                                                                                                                                                                                                                                                                                             DB 4;
                                                                  ----AESWE----S 162
                                                                                                                                                                                               ------MMGELTHR 70
                                                                                                                                                                                                                                                             Indels 109;
                                                                                                                                                                                                                                                                                             Length 529;
                                                                                                                                                                                                                                                           Gaps
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APPLICANT: Chiang, Vincent L
APPLICANT: Chiang, Vincent L
APPLICANT: Smelizer, Richard H
TITLE OF INVENTION: Production of Syringyl Lignin in
FILE REFERENCE: 50617
CURRENT APPLICATION NUMBER: US/08/991,677A
CURRENT FILING DATE: 1997-12-16
EARLIER APPLICATION UNMBER: US 60/033,381
EARLIER FILING DATE: 1996-12-16
NUMBER OF SEQ ID NOS: 11
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US-08-991-677-4
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SEQ ID NO 4
LENGTH: 511
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 10.8%; Score 289; DB 4; Local Similarity 22.0%; Pred. No. 3.6e-20; Local Similarity 95; Mismatches 196;
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LSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDYKKMD
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                                          GSKNSEEVDTDMVDDLLAFYGEEAKVSESDD--
                                                                                                                                                       QL-----KKEYVTFMKGV---VSAPLNLPGTAYHKALQSRATILKFIERKMEERKLDIKE 255
                                                                          EDQEEEEVKTE------DEAEMSKSDHVRKQRTDDDLLGWVLKHSNLSTEQILDLI 305
                                                                                                                   QLFGAFNIADFIPWLKWVPQGINVRLN-------KARGALDGFIDKIIDDH---IQK
                                                                                                                                                                                              -SYRDEVDSAVRVVASNIGSTVNIGELVFALTKNITYRAAFGTISHEDQDEFVAILQEFS 210
                                                                                                                                                                                                                                                                        AD-----MAFAHYGPFWRQMRKLCVMKLFSRKR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                HEALQPLPMTLFFIIPLLLLLGLVSR--LRQRLPYPPGPKGLPVIGNML-MMDQLTHRGL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HHTLLPL-LLLPSLLSLLLFLILLKRRNRKTRENLPPGKSGWPFLGETIGYLKPYTATTL 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 511;
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                                      -LQNSIKLTKDNIKAI
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; Sequence 6, Application US/08948564
; Patent No. 6121512
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                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 919-854-1401 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,092
REFERENCE/DOCKET NUMBER: 5051-409
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-854-1400
TELEFAX: 919-854-1401
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 513 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Corbin, Frederick T.

TITLE OF INVENTION: No. 6121512el Cytochrome P-450 Constructs and NUMBER OF ESQUENCES: 23
CORBERCONTENT: 23
                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
 128
                                 115 SIGGILGKWSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVL-----DSW 168
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                                                                                                                                                                                                      10.4%; Score 279.5; Local Similarity 22.9%; Pred. No. 3.2 hes 118; Conservative 97. ...
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CITY: 1
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                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
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STATE: No. 6121512th Carolina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
 TYGPV---
                                                                                                       VSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPR-----
                                                                  RLKYGSIFTLKMGTRTMIILTDAKLVHEAMIQKGATYATRPPENPTRTIFSENKFTVNAA 127
                                                                                                                                        LAFFISGLIF -- FLKQKSKSKKFNLPPGPPGWPIVGNLFQVARSGKPFF-----EYVNDV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NWELAEDDQP 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PO Box 37428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                    protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       800
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                                                                                                                                                                                                                                                                                                                                                                                             6.
RRNMVQNMLSSTRLKE--FRSVRDNAMDKLINRLKDEAE 173
                                                                                                                                                                                                              Mismatches 216;
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                                                                                                                                                                                                                                               DB 3;
                                                                                                                                                                                                                                               Length 513;
                                                                                                                                                                                                              Indels
                                                                                                                                                                                                              99;
                                                                                                     ----- 114
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CURRENT APPLICATION NUMBER: US/09/144,367;
CURRENT FILING DATE: 1998-08-31;
PRIOR APPLICATION NUMBER: 60/058,612;
PRIOR FILING DATE: 1997-09-10;
NUMBER OF SEQ ID NOS: 58;
SOFTWARE: FastSEQ for Windows Version 3.0;
SEQ ID NO 2;
LENGTH: 503;
TYPE: PRT;
ORGANISM: H. sapiens
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APPLICANT: Lichter, Jay
APPLICANT: Guido, Marco
TITLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
FILE REFERENCE: SEQ-12P
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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RTDDDLLGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREE | | ::|:|| ::|:||
                                                                                                                                             DSWQQNSIFSA--QDEAKKFTFNLMAKHIMS-MDPGEEETEQLKK-EYV-TFMKGVVSAP : | | | | ::| : :: | : | : | : |
                                                                                                                                                                                                  SAISIAEDEEWKRLRSLLSPTFTSGKLKEMVPIIAQYGDVLVRNLRREAETGKPVTL---
                                                                                                                                                                                                                                                                                                           GDFMQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILG--K 122
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                                                      FLIPILEVLNICVFPREVTNFL-RKSVKRMKESRLEDTQKHRV---DFLQL-MIDSQNSK
                                                                                        LNLPGTAYHKALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQ
                                                                                                                                                                                                                                                                       --FDMECHKKYGKVWGFYDGQQPVLAITDPDMIKTVLVKE--CYSVFTNRRPFGPVGFMK
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Pred. No. 1.4e-18;
)1; Mismatches 222;
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US-09-126-420A-18
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SEQ ID NO 18
LENGTH: 504
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TITLE OF INVENTION:
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TITLE OF INVENTION:
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CURRENT APPLICATION NUMBER: US/09/126,420A

CURRENT FILING DATE: 1998-07-30

PRIOR APPLICATION NUMBER: 60/054,351

PRIOR FILING DATE: 1997-07-31

NUMBER OF SEQ ID NOS: 27
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ORGANISM: Solanum melongena
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EPNRKFEDS---
                                   RAKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFL-HRKALKDVRYKGYDIPSGWK 404
                                                                         -----EPAKLSEHEIKIFVLEMFLAGTETTSSSVEWALTELLRHPEAMAKVKTEISQAI
                                                                                                             LLGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIA
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                                                                                                                                                 LKKFDLQSLRKKMARDMGKAVEIMSMFLKE--REEERKKGTEKGKDFLDVLLEFQGTGKD
                                                                                                                                                                                                                                                                                                      -----TAPYGPFWRFQRRICTIEMFVHKKISE--TEPVRRKCVDNMLKWIEKEANSAEK
                                                                                                                                                                                                                                                                                                                                        LGKWSMLVLVGDMHRDMRSI-SLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQD 178
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WERCK-REICHART, DANIELE
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TUBEROSUS AND ITS APPLICATIONS AS BIOCATALYST IN
PARTICULAR FOR THE DEGRADATION OF ENVIRONMENTAL
POLLUTANTS AND FOR ALTERING THE RESISTANCE OF PLANTS S
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APPLICANT: WOON, KYUNG KO
APPLICANT: YOUNG, SOON KIM
TITLE OF INVENTION: A CYTOCHROME P450 GENE HIGHLY EXPRESSED IN:
TITLE OF INVENTION: INCOMPATIBLE INTERACTION
FILE REFERENCE: 10324/P64443USO
CURRENT APPLICATION NUMBER: US/09/499,302A
CURRENT FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 114;
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ORGANISM: Capsicum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---GKWSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDS----WQQNSIF 174
                                      GGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAEDDQPFAFPFVDFPNGLP
                                                                                                       GYDIPSGWKVLPVISAVHLDNSRYDQPNLENPWRWQQQNNGASSSGSGSFSTWGNNYMPF 455
                                                                                                                                                                        LREEHLEIARAKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFL-HRKALKDVRYK 395
                                                                                                                                                                                                                          VQISITDDN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPYGEWT-------RQIRKICILELLSAKM-VKFFSSIRQDELSMMVSSIRTMPNFPV 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLVAFLLFLSSIILLLKKWKTQKLQLPPGPWKLPFIGSL-----FFLAVAGPLPHHGLK 60
   GAGRRICPG-----
                                                                      GYNIPFKTRVIVNAWAIGRDPESWDDPESFSPERF--ENSSVDFLGS------HHQFIPF
                                                                                                                                               AQAEVRQVLKEKK--GFQQIDLDELK---YLKLVIKETLRMHPPIPLLVPRECMKDTKID
                                                                                                                                                                                                                                                           VRKQRTDDDLLGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEE 336
                                                                                                                                                                                                                                                                                               LHDVGGSKTRLLKAHRKIDEILEHVVNEHKQNRADGQKGQGEFGGEDLIDVLLRVRESGE 284
                                                                                                                                                                                                                                                                                                                                   LNLPGTAYHKALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAE----MSKSDH 276
                                                                                                                                                                                                                                                                                                                                                                                                            SAQDEAKKFTFNLMAKHIMSMDPGEEETEQLKKEYVTFMKGVVSAP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 268.5; DB 4
Pred. No. 3.9e-18;
0; Mismatches 208
-MKFG--LANVGQPLAQLLYHFDRKLP
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RESULT 14

RESULT 15 US-09-126-420A-26

Sequence 26, Application US/09126420A Patent No. 6376753 GENERAL INFORMATION:

APPLICANT:

BATARD,

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CURRENT APPLICATION NUMBER: US/09/126,420A

CURRENT FILING DATE: 1998-07-30
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TYPE: PRT
ORGANISM: Solanum melongena
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                                        487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 LFVLDSWQQNSIFSAQD--EAKKF----TFNLMAKHIMSMDPGEEETEQLKKEYVTFMKG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28
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LPHNVSP
                                      LAEDDQP
                                                                                                                    RWQQQNNGASSSGSGSFSTWGNNY--MPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWE 486
                                                                                                                                                                                                                                                                                      FAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDYKKMDFTQC 369
                                                                                                                                                                                                                                                                                                                                                                                                                                  VVSAPLNLPGTA-----YHKALQ-----SRATILKEIERKMEERKLDIKEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRLFECSYPRSIGGILGKWSM-LVLVGDMHRDMRSI-SLNFLSHARL-RTILLKDVERHT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WLKIGSSMNTMVIQTANSASELFRNHDVS-----FSDRPIVDVNLAHNYY-----
                                                                                                                                                                                                                                           LAGTETTSSSVEWALTELLRHPQAMAKVKLEILQVIGPNKKFEECDID-----SLPYVQA 324
                                                                                                                                                                                                                                                                                                                                                                  QEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVL-----KHSNLSTEQILDLILSLL
                                                                              RFLE----
                                                                                                                                                               VLKEQLRLHPPLPLLIPRKAIQDTKFMGYDIPKGTQVLVNAWAIGRDPEYWDNPFEFKPE
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DURST, FRANCIS
WERCK-REICHART, DANIELE
DIDIERJEAN, LUC
NUENTTON
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  441
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os: 27
                                                                              SKVDVKGQNYELIPFGAGRRMCVGLPLGHRMMHFTFGSLLHEFDWE
                                                                                                                                                                                                                                                                                                                              -----KNRSIKDLLDVLIDFEGSGKDEPDKLSEDEIIVIILEMF 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.0%; Score 268; DB 4; 23.2%; Pred. No. 3.9e-18 tive 80; Mismatches 18
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; SEQ ID NO 26
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-126-420A-26
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CURRENT APPLICATION NUMBER: US/09/126,420A

CURRENT FILING DATE: 1998-07-30

PRIOR APPLICATION NUMBER: 60/054,351

PRIOR FILING DATE: 1997-07-31

NUMBER OF SEQ ID NOS: 27
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 VSKYGKIYRSNLFGEPTIV--SADAGLNRFILQNE---GRLFECSYPRSIGGILGKWSML 126
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                                                                                                                                                                          DVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSESTWGN 450 | ::: : : | | :: : : | | :: : | | : | | : | | : | | : | | : | | : | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | : | | | | : | | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
AFVPFSIGKRYCFGEGLARMELFLFLINIMQNFCFKSPQAPQDIDVSPRLVGFATIP 484
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                                                                                                                                                                                                                                                                                                                                                              IEAKVHEE-----IDRVIGRNRQAKYEDRMKMPYTEAVIHEIQRFADMIPMGLARRVTK 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---HLPG-PQQQAFKELQGLEDFITKKVEQNQRTLD-------PNSPRDF 267
                                                                                       NYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAE-----DDQPFAFPFVDFP 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             I-----DSFLIRMLEEKKNPNTEFYMKNLVLTTLNLFFAGTETVSTTLRYGFLLLMRHPD
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DURST, FRANCIS
WERCK-REICHART, DANIELE
DIDIERJEAN, LUC
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./cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep: *
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./cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep: *
./cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 2 3 3 4 4 4 6 6 7 7 7 11 11 11 11 11 11 11 11 11 11 11	Result No.
290.5 290.5 290.5 290.5 285.5 285.5 285.5 255.5 256.7 256.7 251 251 251 249 249 249 249 249	Score
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Sequence 3, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 69, Appl Sequence 69, Appl Sequence 10, Appl Sequence 11, Appli Sequence 12, Appli Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli Sequence 18, Appli Sequence 3, Appli	Description

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Sequence 264,	Sequence 264,	Sequence 264,		Sequence 264,	Sequence 264,	Sequence 905,	Sequence 905,	Sequence 108,		Sequence 108,														
App	App	App	Appl	App	App	, Ap	App																	

ALIGNMENTS

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72 1 74 126 : 130 182 :	t Local ches	RESULT 1 US-10-067-534-3 Publication K GENERAL INFORM APPLICANT: E APPLICANT: E APPLICANT: I TITLE OF INV FILE REFEREN CURRENT FILI CURRENT FILI PRIOR APPLICA OF SOFTWARE: Fa SEQ ID NO 3 SEQ ID NO 3
72 VSKYGKIYRSNLFGEPTIVSADAGINRETIQNEGRIFECSYPRSIGGILGKWSM 125 :	Query Match 10.9%; Score 292; DB 9; Length 516; Best Local Similarity 23.6%; Pred. No. 7.8e-16; Best Local Similarity 23.6%; Pred. No. 7.8e-16; Matches 120; Conservative 92; Mismatches 220; Indels 76; Gaps 17; 12 LLLLPSLLSLLLFLILLKRNNKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDFMQQH 71 13	SULT 1 -10-067-534-3 -10-067-534-3 -10-067-534-3 -110-067-534-3 -110-067-534-3 -110-067-534-3 -110-067-534-3 -110-067-534-3 -110-067-534-3 -110-067-534-3 -110-067-534-3 -110-067-534-3 -110-067-534-3 -110-067-534-3 -110-067-534-3 -110-067-534-3 -110-067-534-3
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SEQ ID NO 4
LENGTH: 514
TYPE: PRT
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APPLICANT: Chiang, Vincent Lee C.
APPLICANT: Li, Laigeng
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CURRENT APPLICATION NUMBER: US/09/947,027
CURRENT FILING DATE: 2001-09-05
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TITLE OF INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGNIN CONTENT AND COMPOSITIC
TITLE OF INVENTION: CELLULOSE CONTENT IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/230,086 PRIOR FILING DATE: 2000-09-05
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Local Similarity 22.6%;
les 123; Conservative 98
KAVEELREEHLEIARAKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKD
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                                                                                           FIPWLGWIDPQGLSARLVK--ARKALDRFIDSIIDDHIQKRKQNKFSEDAETDMVDDMLA
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                                FYGEEARKVDESDDL----QKAISLTKDNIKAIIMDVMFGGTETVASAIEWVMAELMKSP
                                                   ----HYRKQRTDDDLLGWYLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACP 331
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Pred. No. 1e-15;
98; Mismatches 230; Indels 93;
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
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TITLE OF INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGNIN CONTENT TITLE OF INVENTION: COMPOSITION, AND
TITLE OF INVENTION: COMPOSITION, AND
TITLE OF INVENTION: CELLULOSE CONTENT IN PLANTS
FILE REFERENCE: 066040-9718
CURRENT APPLICATION NUMBER: US/10/091,009
CURRENT TILING DATE: 2002-03-06
PRIOR ADDITIONS.
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PRIOR FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: 60/230,086
PRIOR FILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: aspen populus tremuloides
                                                           332 KAVEELREEHLEIARAKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKD 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        500 TRLV 503
                                                                                                                                                                                                                                                                                                       222 NLPGTAYHKALQSRATILKFIERKMEERKLD--IKEEDQEEEEVKTEDEAEMSKSD----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 PLLLLPSLLSLLLFLILLKRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDFMQQ 70
EDQKRVQQELAEVVGLERRVEESDID-----KLTFLKCALKETLRMHPPIPLLLHETSED
                                                                                                                                                                              ----HVRKQRTDDDLLGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACP 331
                                                                                                                                                                                                                                                                                                                                                                                                                       LEVIDSWQQNSIFSAQDEAKKFTFNLMAKHIMSMDPGEEETEQLKKEYVTFMKGVVSAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---MAFAHYGPFWRQMRKLCVMKLFSRKRAESWESVRDEVDSMLKTVEANIGKPVNLGEL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEFIPFGSGRRSCPGMQLGLYTLDLAVAHLLHCFTWELPDGMKPSELDMTDMFGLTAPRA
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                                                                                                                         FYGEEARKVDESDDL----QKAISLTKDNIKAIIMDVMFGGTETVASAIEWVMAELMKSP
                                                                                                                                                                                                                                            FIPWLGWIDPQGLSARLVK--ARKALDRFIDSIIDDHIQKRKQNKFSEDAETDMVDDMLA
                                                                                                                                                                                                                                                                                                                                                                  IFTL---TMNITYRAAFGAK------NEGQDEFIKILQEF-SKLFGAFNMSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYSKYGKIYRSNLFGEPTIYSADAGLNRFILQNEGRLFE------CSYPRSIGGIL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PMSLFLIVISSLFFFGLLSRLRR--RLPYPPGPKGLPLVG-SMHMMDQITHRGLAKLAKQ
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359 YLKCVLKEVLRLHPPIPLLLHETAEDAEVGGYYIPAKSRVMINACAIGRDKNSWADPDTF
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                                                                                                                                                        306 LSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDYKKMD 365
                                                                                                                                                                                            258 GSKNSEEVDTDMVDDLLAFYGEEAKVSESDD------LQNSIKLTKDNIKAI
                                                                                                                                                                                                                         256 EDQEEEEVKTE-----DEAEMSKSDHVRKORTDDDLLGWVLKHSNLSTEQILDLI 305
                                                                                                                                                                                                                                                       211 QLFGAFNIADFIPWLKWVPQGINVRLN------KARGALDGFIDKIIDDH---IQK 257
                                                                                                                                                                                                                                                                                                                          152 - SVRDEVDSAVRVVASNIGSTVNIGELVFALTKNITYRAAFGTISHEDQDEFVAILQEFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 AKLAKQ----YGGLEHLKMGFLHMVAVSTPDMARQVLQVQDNIFSNRPATIAISYLTYDR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 HEALQPLPWTLFFIIPLLLLLGLVSR--LRQRLPYPPGPKGLPVIGNML-MMDQLTHRGL 62
                                                                                      FTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLF 425
                                                                                                                           MDVMFGGTETVASAIEWAMTELMKSPEDLKKVQQELAVVVGLDRRVBEK-----DFEKLT 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 HHTLLPL-LLLPSILSLILLFLILLKRRNRKTRENLPPGKSGWPFLGETIGYLKPYTATTL 64
                                                                                                                                                                                                                                                                                         QL-----KKEYVTFMKGV---VSAPLNLPGTAYHKALQSRATILKFIERKMEERKLDIKE 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     440 FEFTPFGSGRRSCPGMQLGLYTLDLAVAHLLHCFTWELPDGMKPSELDMTDMFGLTAPRA 499
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; OTHER INFORMATION: Xaa equals stop translation
US-09-739-254-69
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Best Local Similarity
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SEQ ID NO 69
LENGTH: 502
TYPE: PRT
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389 LKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSESTW 448
                                                  329 YPNIQGQVQKE-IDLIMGP----NGKPSWDDKCKMPYTEAVLHEVLRFCNIVPLGIFHAT 383
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EARLIER FILING DATE: 2000-02-23
EARLIER APPLICATION NUMBER: PCT/US99/19330
EARLIER FILING DATE: 1999-08-24
EARLIER APPLICATION NUMBER: 60/097,917
PARTITUD TATES. 1008-00-26
                                                                           GENERAL INFORMATION
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                                                                                                                  285 DOGKND-----PSSTFSKENLIFSVGELITAGTETTINVLRWAILFMAL
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EARLIER APPLICATION NUMBER: 60/
EARLIER FILING DATE: 1998-08-31
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CURRENT FILING DATE: 2000-12-19
                                                                                                                                               270 EMSKSDHVRKQRTDDDLLGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQA 329
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                                                                                                                                                                                 225 SVELYNAFPWIGILPFGKHOOLFRNAAVVYDFLSRLIEKASVNRKPOLPOHFVDAYLDEM 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                               174 FSAQDEAKK---FTENLMAKHIMS-----MDPGE----EETE-----QLKKEYYTENKGV 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rosen et al.
TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: PZ032P1
                                                                                                                                                                                                                                                                                                               124 LLNSRYGRGWV------DHRRLAVNSFRYFGYGQ------KSFESKIL------EETKF 164
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                                                                                                                                                                                                                                                                                                                                                                                                              67 FMQQHVSKYGKIYRSNLFGEPTIYSADAGLNRFIIQNEGRLFECSYP-----RSIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                14 LGGALFILLFALGVRQLLKQRR----PMGFPPGPPGLPFIGNI-----YSLAASSELPHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 LPSTLSTLLFLI----LIKRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGD----
                                                                                                                                                                                                                VSAPLN-----LPGTAYHKALOSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEA 269
                                                                                                                                                                                                                                                FNDAIETYKGRPEDEKQLITNAVSNITNLIIFGERETYEDTDEQHMIELESENVELAASA 224
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                                                                                                                                                                                                                                                                                                                                               ILGK-----WSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSI 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.6%; Score 285.5; DB LU; 23.4%; Pred. No. 2.6e-15; ac. Mismatches 210;
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LENGTH: 511
TYPE: PRT
ORGANISM: Liquidambar styraciflua
US-09-796-256A-4

NUMBER OF SEQ ID NOS: 11
SOPTWARE: Patentin Ver. 2.1
LPNOW.

PRIOR FILING DATE:

CURRENT APPLICATION NUMBER: US/09/796,256A CURRENT FILING DATE: 2001-02-28

PRIOR APPLICATION NUMBER: US60/033381 PRIOR FILING DATE: 1996-12-16

APPLICATION NUMBER: 08/991677

US-09-796-256A-4

GENERAL

INFORMATION:

Sequence 4, Application US/09796256A Patent No. US20020078477A1

APPLICANT: Carraway, Daniel T APPLICANT: Smeltzer, Richard H APPLICANT: Chiang, Vincent L 밁 Ş

500 TRLV 503

510 SRIL 513

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Query Match Best Local Similarity

Matches

121;

Conservative

10.8%; Score 289; DB 10; 22.0%; Pred. No. 1.4e-15; tive 95; Mismatches 196;

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Best Local :
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LENGTH: 502
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APPLICANT: ROSEN et al.
APPLICANT: ROSEN et al.
TITLE OF INVENTION: 49 Human Secreted
FILE REFERENCE: PZ032P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 69, Application US/09904615 Patent No. US20020026040A1
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PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/097,917
PRIOR FILING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: 60/098,634
PRIOR APPLICATION NUMBER: 60/098,634
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CURRENT FILING DATE: 2001-07-16
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NUMBER OF SEQ ID NOS: 170
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NAME/KEY: SITE
LOCATION: (502)
OTHER INFORMATION: Xaa equals stop translation
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Local Similarity 23.4%;
GNNYMPFGGGPRLCAGSELAKLEMAVFIHHLV----LKFNWELAEDDQP 493
                                                        SEDAVVRGYSIPKGTTVITNLYSVHFDEKYWRDPEVFHPERF------LDSSGYFAK-
                                                                                              LKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTW
                                                                                                                                                       CPKAVEELREEHLEIARAKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRF-LHRKA
                                                                                                                                                                                                                                   EMSKSDHVRKQRTDDDLLGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQA
                                                                                                                                                                                                                                                                                       SVFLYNAFPWIGILPFGKHQQLFRNAAVVYDFLSRLIEKASVNRKPQLPQHFVDAYLDEM
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                                                                                                                                 YPNIQGQVQKE-IDLIMGP----NGKPSWDDKCKMPYTEAVLHEVLRFCNIVPLGIFHAT
                                                                                                                                                                                                                                                                                                                        VSAPLN-----LPGTAYHKALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEA
                                                                                                                                                                                                                                                                                                                                                               FNDAIETYKGRPFDFKQLITNAVSNITNLIIFGERFTYEDTDFQHMIELFSENVELAASA 224
                                                                                                                                                                                                                                                                                                                                                                                                 FSAQDEAKK----FTFNLMAKHIMS-----MDPGE----EETE-----QLKKEYVTFMKGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -WSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSI 173
                                                                                                                                                                                                            -----PSSTFSKENLIFSVGELITAGTETTTNVLRWAILFMAL
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US-09-945-301-4
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US-10-067-668-10
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APPLICANT: Glucksmann, Maria Alexandra
TITLE OF INVENTION: 33312, 33303, 32579, NOVEL HUMAN
TITLE OF INVENTION: CYTOCHROME P450 FAMILY MEMBERS AND USES THEREOF
FILE REFERENCE: 10448-136001
CURRENT APPLICATION NUMBER: US/10/067,668
CURRENT FILING DATE: 2002-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
RNCLGERLARMELFLFLATLLQRF-----PELELAVPPGDIPSLTPKPELGLP
                                                                                                                                                                            LEIARAKKELGESELNWDDYKKMDFTQCVINETLRLGNVV-RFLHRKALKDVRY-KGYDI 399
                                                                                                                                                                                                                                                    TDDDLLGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEH
                                  RLCAGSELAKLEMAVFIHHLVLKFNWELAEDDQPFAFPFVDFPN-----GLP 506
                                                                                                            PSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGP 459
                                                                                                                                                                                                                              KAAKDLKDYLDKLIEERRETLEPAGDPRRLDIGFLDSLLLEAKREGGNPKSE------
                                                                                                                                                                                                                                                                                                                                            QSRATILKFIERKMEE------RKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQR
                                                                                                                                                                                                                                                                                                                                                                                    V----REDYLRPEDPEFLK-LIDKLLNEMFDRVSPWHQLLDIFPFLLRYLPGSLFRKAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGLINEFILQNEGRL-----FECSYPRSIGGILGKWSMLVLVGDMHRDMRSISLNFL-- 144
                                                                          PKGTLVIVNLYSLHRDPKVFPNPEEFDPERFLDENGKFKKSYA-----FLPFGAGP
                                                                                                                                                    DEVIGRDR----SPTYDVDARAQMPYLDAVIKETLRLYPVVPLLLPRVATKDTEIPDGYLI
                                                                                                                                                                                                                                                                                                                                                                                                                        MDPGEEETEQLKKEYVTFMKGVVSAPLN--------------------LPGTAYHKAL 232
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Pred. No. 1.8e-14;
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Sequence 4, Application US/09945301 Patent No. US20020090699A1 GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceutic

Millennium Pharmaceuticals,

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RESULT 9
US-10-067-668-12
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                                                                                                                                             Sequence 12, Application US/10067668 Publication No. US20030022334A1 GENERAL INFORMATION:
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                                                                   APPLICANT: Glucksmann, Maria Alexandra
TITLE OF INVENTION: 33312, 33303, 32579, NOVEL HUMAN
TITLE OF INVENTION: CYTOCHROME P450 FAMILY MEMBERS
FILE REFERENCE: 10448-136001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: 27439, NOVEL HUMAN HYI
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 38155-20036.00
CURRENT APPLICATION NUMBER: US/09/945,301
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,301
PRIOR FILING DATE: 2000-09-01
CURRENT APPLICATION NUMBER: US/10/067,668
CURRENT FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: 60/266,140
PRIOR FILING DATE: 2001-02-02
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                                                                                                                                                                                                                                                                                                               RLCAGSELAKLEMAVFIHHLVLKFNWELAEDDQPFAFPFVDFPN-----GLP 506
                                                                                                                                                                                                                                                                                                                                                                                     PSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGP 459
                                                                                                                                                                                                                                                                                                                                                                                                                           DEVIGEDR----SPTYDVDARAQMPYLDAVIKETLRLYPVVPLLLPRVATKDTEIPDGYLI
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                                                                                                                                                                                                                                                                            RNCLGERLARMELFLFLATILQRF-----PELELAVPPGDIPSLTPKPELGLP 483
                                                                                                                                                                                                                                                                                                                                                  PKGTLVIVNLYSLHRDPKVFPNPEEFDPERFLDENGKFKKSYA-----FLPFGAGP
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Tsai, Fong-Ying
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Pred. No.
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                                                                                                            NOVEL HUMAN
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US-09-992-901-2
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                                                                                                                        ; ORGANISM: Arabidopsis thaliana US-09-992-901-2
                                                                                                                                                                       SOFTWARE: FastSEQ
SEQ ID NO 2
LENGTH: 520
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SOFTWARE: FastSEQ for
SEQ ID NO 12
                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09992901 Patent No. US20020073446A1
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                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chory, Joanne
TITLE OF INVENTION: GENETICALLY MODIFIED PLANTS HAVING
TITLE OF INVENTION: MODULATED BRASSINOSTEROID SIGNALING
FILE REFERENCE: SALKINS.024DV1
                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/172,832 PRIOR FILING DATE: 1999-12-20
                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/124570 PRIOR FILING DATE: 1999-03-16 PRIOR APPLICATION NUMBER: US 60/170,931 PRIOR FILING DATE: 1999-12-14
                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/992,901
CURRENT FILING DATE: 2001-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Neff, Michael M. APPLICANT: Chory, Joanne
                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 09/527,073 PRIOR FILING DATE: 2000-03-16
                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                          TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     332 KAVEELREEHLEIARAKKELGESELNWDDYKKMDFTQCVINETLRLGNVV-RFLHRKALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          272 SKSDHVRKQRTDDDLLGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 LPGSLFRKAFKAAKDLKDYLDKLIEERRETLEPAGDPRRLDIGFLDSLLLEAKREGGNPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223 LPGTAYHKALQSRATILKFIERKMEE-------RKLDIKEEDQEEEEVKTEDEAEM 271
                                                  y Match 9.6%;
Local Similarity 23.8%;
hes 136; Conservative 9
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1 MFETEHHTLLPLILLLPSLLSLLLFLILLKR-----RNRKTRFNL-PPGKSGWP---FLG
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                                                                                                                                                                                                           for Windows Version 4.0
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                                                  Score 256.5; 1
Pred. No. 6.3e
95; Mismatches
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                                                  6.3e-13;
ches 225;
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                                                                                    DB 10;
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US-09-796-138-19
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US-09-796-138-19
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SEQ ID NO 19
LENGTH: 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19, Application US/09796138 Patent No. US20020031782A1
                                                                                                                               Matches 120;
                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Mycobacterium tuberculosis CYP51 HIGH RESOLUTION STUCTURE, TITLE OF INVENTION: AND TITLE OF INVENTION: NUCLEIC ACIDS, AND THERAPEUTIC AND SCREENING METHODS TITLE OF INVENTION: RELATING TO SAME FILE REFERENCE: ACTORY DOCKET NO. US20020031782A1 1242-17-2 CURRENT APPLICATION NUMBER: US/09/796,138 CURRENT FILING DATE: 2001-02-28
                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/345,218 PRIOR FILING DATE: 1999-06-30 NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Waterman, Michael R.
                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Penicillium italicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                485
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                                                                                                                                                 Local Similarity
                                                              LLLLPSLLSLLLFLILLKRRNRKTRENLPPGKSGW-PFLGETIGY-LKPYTATTLGDFMQ 69
QHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TFHLAPTYQHAPTVLMLLYPQHGAPITFRRL 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKF 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSNLSTEQILDLI
                                     LFLVSIVLNVIKQLIFYNRKE-----PPVVFHWIPFIGSTIAYGMDPY-----QFFF 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EFNPARFADGVPRAAKHPVG-----FIPFGLGVRTCIGQNLAILQAKLTLAVMIQRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NVKELVGMMLKASSHPMPFSHNILPRVLSFY-HHWRKIYGATFLVWFG-PTFRLTVADPD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEEESSSWFIPKVL---VLSVILSLVIVKGMSLLWWRPRKIEEHFSKQGIRGPPYHFFIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Podust,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bellamine, Aouatef
Podust, Larissa M.
                                                                                                                             Conservative
                                                                                                                                        9.48;
22.78;
                                                                                                                          ; Score 251; DB 10;
; Pred. No. 1.8e-12;
75; Mismatches 213;
                                                                                                                                                                  Length 515;
                                                                                                                          Indels 120;
                                                                                                                        Gaps
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
SEQ ID NO 19
LENGTH: 515
TYPE: PRT
ORGANISM: Penicillium italicum
US-09-909-903-19
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US-09-909-903-19
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Patent No. US20020052031A1
GENERAL INFORMATION:
APPLICANT: Waterman, Michael R.
APPLICANT: Bellamine, Aouatef
                                                                                                                                                                                                                                                                                                                                                              Query Match 9.4%; Score 251; DB 10; Best Local Similarity 22.7%; Pred. No. 1.8e-12; Matches 120; Conservative 75; Mismatches 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Mycobacterium tuberculosis CYP51 POLYPEPTIDES TITLE OF INVENTION: NUCLEIC ACIDS AND THERAPEUTIC AND SCREENING M TITLE OF INVENTION: RELATING TO SAME FILE REFERENCE: Attorney Docket No. US20020052031A1 1242-17 CURRENT APPLICATION NUMBER: US/09/909,903 CURRENT FILING DATE: 2001-07-20
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                 176 TIDLAAAMAEITIFTAARTLQ----GEEVRSKLTSEFADLFHDLDLGFSPINFMLPWAPL
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                                                       -----KFTFNLMAKHIMSMDPGEEETEQLKKEY------VTFMKGVVSA
                                                                                                  SDVVYDCPNSKLMEQKKFIKYGLSQEAL----ESYVPLIAD--ETNAYIKSSPNFKGQSG
                                                                                                                                            GDMHRDMRSISL----NFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAK----
                                                                                                                                                                                       ASRAKYGDIFTFILLGKKTTVYLGVEGNEFIL--NGKLKDVNAEE----VYGKLTTPVFG
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Sequence 8, Application US/10067668

Publication No. US20030022334A1

GENERAL INFORMATION:
APPLICANT; GLUCKSMAND, MARIA ALEXANDRA
TITLE OF INVENTION: 33312, 3303, 32579, NOVEL HUMAN
TITLE OF INVENTION: CYTOCHROME P450 FAMILY MEMBERS AND
FILE REFERENCE: 10448-136001
FILE REFERENCE: 10448-136001
CURRENT APPLICATION NUMBER: US/10/067,668
CURRENT FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: 60/266,140
PRIOR APPLICATION NUMBER: 60/266,140
PRIOR APPLICATION NUMBER: 60/266,140
PRIOR FILING DATE: 2001-02-02

NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8
LENGTH: 544
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                                                                                                EMSKSDHYRKQRTDDDLLGWYLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQA
                                                                                                                                                      QVLLVNICPWLYYLPFGPFKELRQIEKDITSFL-----KKIIKDHQESLDRENPQDFI
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  NPDVQEKVHEEIERVIGANR-----APSLTDKAQMPYTEATIMEVQRLTVVVPLAIPHMT
                                  CPKAVEELREEHLEIARAKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRF-LHRKA
                                                                          DMYLL-HMEEERKNN-----SNSSFDEEYLFYIIGDLFIAGTDTTTNSLLWCLLYMSL
                                                                                                                                                                                                                              MQKH----GEDPFCPFSIISNAVSNIICSLCFGQRFDYTNSEFKKMLGFMSRGLEICLNS
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No. 1.9e-12;
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Matches
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 503
TYPE: PRT
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TITLE OF INVENTION: AND
TITLE OF INVENTION: NUCLEIC ACIDS, AND THERAPEUTIC AND SCREENING METHODS
TITLE OF INVENTION: RELATING TO SAME
FILE REFERENCE: Attorney Docket No. US20020031782A1 1242-17-2
CURRENT APPLICATION NUMBER: US/09/796,138
CURRENT FILING DATE: 2001-02-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 9.3%; Score 249; DB 10; Local Similarity 24.1%; Pred. No. 2.5e-12; National Conservative '87; Mismatches 212;
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  KGYDIPSGWKYL--PYISAVHLDN--SRYDQPNLENPWRWQQQNNGASSSGSGSFSTWGN
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                                                            -KKCYLE----QKTVCGENLPPLTYDQLKDLNLLDRCIKETLRLRPPIMIMMRMARTPQTV
                                                                                              LREEHLEIARAKKELGES--ELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRY
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Sequence 18, Application US/0990903
Patent No. US20020052031A1
GENERAL INFORMATION:
APPLICANT: Waterman, Michael R.
APPLICANT: Hellamine, Aouatef
TITLE OF INVENTION: Mycobacterium tuberculosis CYP51 POLYPEPTIDES AND
TITLE OF INVENTION: MYCOBACTERIUM THERAPEUTIC AND SCREENING METHODS
TITLE OF INVENTION: RELATING TO SAME
TITLE OF INVENTION: RELATING TO SAME
FILE REFERENCE: Attorney Docket No. US20020052031A1 1242-17
CURRENT APPLICATION NUMBER: US/09/909,903
CURRENT FILING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
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                                         -YVPFGAGRHRCIGENFAYVQIKTIWSTMLRLYEFDLIDG----YFPTVNYTTMIHTPEN 493
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Search completed: March 30, 2003, 12:14:58 Job time: 54 secs

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KTEDEAEMSKSDH LFFLQACPKAVEEI LFFLQACPKAVEEI	QLKKEYVTFMKGV KKEYVTFMKGV 	FGEPTIVSADAGL LSHARLRTILLKD SHARLRTILLKD	FILLLKRRNKTH FILLLKRRNKTH FILLLKRRNRKTH FILLLKRRNRKTH FILLLKRRNRKTH FILLLKRRNRKTH	Score 2677; Pred. No. 1.1 1; Mismatches	## 50	Ϋ́	79 Columbia; BAC	r, K.F.X.; Database,	Arab ear	ALIGNMENTS	T24780 JC4702 S38534 T04735	A27491 T05246 A29410 AG1987	D96672 T48140 O4RTPB S35666	S27160 A31047 A33293 O4RBPC
FIEKKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKORTDDDLLGWVLKHSNLSTEQ 300 ILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDD 360		GKWSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAGDEA 180		2677; DB 2; Length 513; No. 1.1e-165; smatches 0; Indels 0; Gaps	0 slr0574; cytochrome P450 homology <p45> ligand) #status predicted</p45>		clone T3A5	Lemcke, K.; Schueller, C.; Quetier December 1999	ldopsis thaliana cress) Feb-2000 #text_change 16-Feb-2001	ัด	hypothetical prote cytochrome p450 3A cytochrome p450 76 cytochrome p450 ho	lanosterol 14alph cytochrome P450 n cytochrome P450,		cytochrome P450 2B testosterone 16alp cytochrome P450 2A cytochrome P450 2A
				0;	Ϋ́Ð			ler, F.;			10 te	mo ha	rom hy 28	28 11p 2A

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A;Gene: CYP90
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;
F;275-440/Domain: cytochrome P450 homology <P45>
F;418/Binding site: heme iron (Cys) (axial ligand) #status predicted
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A; Residues: 1-472 <SZE>
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A; Accession: S55379
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R;Szekeres, M.; Nem
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N;Contains: oxidoreductase (EC 1.-.-)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
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  DQPFAFPFVDFPNGLPIRVSR
                                                                                                                                          GYETTSTIMTLAVKFLTETPLALAQLKEEHEKIRAMKSD--SYSLEWSDYKSMPFTQCVV
                                                                                                                                                            GHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDYKKMDFTQCVI 371
                                                                                                                                                                                                                                                                         IMSMDPGEEETEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILKFIERKMEERKL 251
                                                                                                                                                                                                                                                                                                                                 MHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAKKFTFNLMAKH 191
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                                                                                    NETLRVANIIGGVFRRAMTDVEIKGYKIPKGWKVFSSFRAVHLDPNHFKDARTFNPWRWQ
                                                                                                    NETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQ 431
                                                                                                                                                                                                                             DIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSNLSTEQILDLILSLLFA 311
                                                                                                                                                                                                                                                         LMSFDPG-EWSESLRKEYLLVIEGFFSLPLPLFSTTYRKAIQAR-----RKVAEALT
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                                                                                                                                                                                                                                                                                                                                                                                                  VSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLVGD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                LLLLSSIAAGFL---LLLRTRYRRMGLPPGSLGLPLIGETFQLIGAYKTENPEPFIDER 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210;
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    SNSVTTGPSNVFTPFGGGPRLCPGYELARVALSVFLHRLVTGFSWVPAEQ

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Pred. No. 7.5e-56;
9; Mismatches 171;
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A:Map position: 1
C:Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450
C:Keywords: heme; iron; metalloprotein
{ F: 455/Binding site: heme iron (Cys) (axial ligand) #status predicted
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R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; ansen, N.F.; Hughes, B.; Huizar, L.

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, A; Authors: Hinter, J.L.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.

A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Reference number: A86141; MUID:21016719; PMID:11130712
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A; Residues: 1-512 <STO>
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GGTRFCPGAELARLQIALFLHYFITTYKWTQLKEDRISFFPSARLVNGFKIQLNR
                                                                 GGPRLCAGSELAKLEMAVFIHHLVLKFNWELAEDDQPFAFPFVDFPNGLPIRVSR
                                                                                                                                                                                                          GCFVVPFLSAVHLDESYYKESLSFNPWRWLDPETQQKRNWRTSP--
                                                                                                                                                                                                                                                                                                             GWKVLPVISAVHLDNSRYDQPNLFNPWRW-----QQQNNGASSSGSGSFSTWGNNYMPFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEIARAKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPS 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LQTLSNFKDGEVVLLQDICRKVAIHLMVNQLLGVS-SESEVDEMSQLFSDFVDGCLSVPI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QNEGKLFQSSYPKSFRDLVGKDGVITVHGDQQRRLHSIASSMMRHDQLKTHFLEVIPVVM 190
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Pred. No. 1.6e-
05; Mismatches
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..6e-48;
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C;Accession: T48613
R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, submitted to the Protein Sequence Database, /
                                                             RESULT 5
748613
hypothetical protein F18022.190 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Species: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
A; Reference number: 224493
A; Accession: T48613
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C; Keywords: heme; ir
F; 396/Binding site:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:NC_001268; NID:g7270586; PIDN:CAB80304.1; GSPDB:GN00140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-457 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: D85429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Nature 402, 769\text{-}777, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytochrome P450 like protein [imported] - Arabidopsis thaliana (C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 *sequence_revision 16-Feb-2001 *text_change 02-Apr-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
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                                                                                                                                                                                                                     IRVATV 445
                                                                                                                                                                                                                                                                                  ----FTPFGGGQRLCPGLELSKLEISIFLHHLVTRYSW-TAEEDEIVSFPTVKMKRRLP
                                                                                                                                                                                                                                                                                                                   TWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAEDDQPFAFPFVDFPNGLP
                                                                                                                                                                                                                                                                                                                                                          KALKDVEIKGYLIPKGWCVLASFISVHMDEDIYDNPYQFDPWRWDRINGSANSSIC----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEAEMSKSDHVRKQRTDDDLLGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFF 326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLVGDMHRDMRSISLNFLSHARLRTI 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPNGSLGWPVIGETLNFIACGYSSRPVT-----FMDKRKSLYGKVFKTNIIGTPIIIST
                                                                                                                                                                                                                                                         IRVSRI 512
                                                                                                                                                                                                                                                                                                                                                                                                                                 LSDNPVALAKLVEENMEMKRRKLELGE-EYKWTDYMSLSFTQNVINETLRMANIINGVWR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DAEVNKYVLQNHGNTFVPAYPKSITELLGENSILSINGPHQKRLHTLIGAFLRSPHLKDR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179;
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3; Mismatches 160;
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                              , S.; Bancroft,
April 2000
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12 LLLLPSLLSLLLFLILLKRRN--RKTRFNLPPGKSGWPFLGETIGYLKPYTATTLG-DFM

Matches

Conservative

90;

Mismatches

188;

Indels

61;

Gaps

10;

5

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Oy
                                                                                                 A;Cross-references: EMBL:U54770; NID:g1421740; PIDN:AAB17070.1; PID:g1421741
A;Experimental source: strain GCR758
C;Genetics:
                                                                                                                                                                                     A;Reference number: Z16181; MUID:96266705; A;Accession: T07859
                                                                                                                                                                                                                    R;Bishop, G.J.; Harrison, K.; Jones, J.D. plant Cell 8, 959-969, 1996
A;Title: The tomato Dwarf gene isolated b
                                                                                                                                                                                                                                                                             cytochrome P450 homolog - tomato
C:Species: Lycopersicon esculentum (tomato)
C:Date: 14-May-1999 #sequence_revision 14-May-1999
                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-464 <BIS>
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A; Introns: 31/2; 1:
A; Note: F18022.190
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-382 <BEV>
A;Cross-references: EMBL:DB
A;Experimental source: cultivar Columbia; BAC clone F18022
C;Genetics:
                                           Superfamily: Synechocystis cytochrome P450 slr0574; 273-436/Domain: cytochrome P450 homology <P45>
                                                                                   Gene: dwarf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -RAKKGDGEL-LNWEDYQKMEFTQCVISEALRCGNIVKTYHRKATHDIKFNEYVIPKGWK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGYTNAIKVRSNRNIHQNAIIEDMNNAIREEDFLDSIISNED----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GWPFIGETISFFKPHRSDSIGTFLQQRVSRYGKVFKSNICGGKAVVSCDQELNMFILQNE 61
 Similarity
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 28.4%;
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Score 761.5; DB 2
Pred. No. 7.9e-42;
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Pred. No. 2.1e-45;
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                                                                                                                                                                       GB/EMBL/DDBJ
                                                                                                                                                                                                  heterologous
PMID:8672892
           DB 2;
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                                                          cytochrome
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             Length
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                                                          P450
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A;Introns: 67/2; 173/3; 302/3; 358/1; 393/3
A;Note: T18B16.200; T5K18.10
C;Superfamily: Synechocystis cytochrome P450 slr0574;
C;Keywords: chromoprotein; electron transfer; heme; ir
F;272-433/Domain: cytochrome P450 homo
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                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-457 <BEV>
A; Cross-references: EMBL; AL021687
                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytochrome P450 - Arabidopsis thaliana Wildernate names: protein T18B16.200; protein T5K1 N;Contains: oxidoreductase (EC 1.-.-.)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999
C;Accession: T04444; T05806
C;Accession: T04444; T05806
                                                                                                                                                                                             A; Experimental source: cultivar Columbia; BAC C; Genetics:
                                                                                                                                                                                                                                        A; Molecule type: DNA
A: Residues: 131-457 <BEW>
                                                                                                                                                                                                                                                                         A; Reference number: Z15453
A; Accession: T05806
                                                                                                                                                                                                                                                                                                      A; Experimental source: cultivar Columbia; BAC clone T18B16 R; Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; submitted to the Protein Sequence Database, April 1998
                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the Protein Sequence A; Reference number: Z15359
A; Accession: T04444
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                                                                                                                                                                                                                             A; Cross-references: EMBL: AL022580
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 13
                                                 Local
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LLLPSLLSLLLFLILLKRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDFMQQHV 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KFNWELAEDDQPFAFPFVDFPNGLPIRVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKYLPVISAVHLDNSRYDQ : | || : | | | || :: : | | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AKHIMSMDPGEEET---EQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILKFIERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KYRWEEIGGDKLMKFPRVEAPNGLRIRVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHS----NLSTEQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKQI----AGIESTSLAQEFMSEFFNLVLGTLSLPINLPNTNYHRGFQARKIIVNLLRTL
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                                                 Similarity
                                 Conservative
                                              23.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    S.; Borkova, D.; Ansorge, W.;
Database, April 1998
                                              Score 632;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LEHQNSFLVFGGGTRQCPGKELGVAEISTFLHYFVT
    DB 2;
... No. 1.8e-33;
Mismatches 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein T5K18.10
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                                                                                                                                                                                                            clone T5K18
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                                                                                                            iron;
                                                                                                            cytochrome P450 homology
ron; monooxygenase; oxidoreductase
                                 Indels
                                                                                                                                                                                                                                                                                                                        Robben, J.; Volckaert,
                             56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bancroft, I.;
                             Gaps
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                                                                                                                                                                           A; Gene: At2g29090;
                                                                                                                                                                                        C; Genetics:
                                         Query Match
Best Local S
Matches 153
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             PSLLSLLLFLILLK-----RRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDFMQ 69
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: I-482 <ROU>
A;Cross references: EMBL:AC005315; NID:g3461834; PID:g3461849
A;Experimental source: cultivar Columbia
R;Ein, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.;
M.; KOO, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.
Nature 402, 761-768, 1999
                                                                                                                   A;Map position: 2
A;Introns: 80/2; 187/3; 238/3; 321/3; 351/3; 413/3; 453/2
A;Introns: 80/2; 187/3; 238/3; 321/3; 351/3; 413/3; 453/2
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome F;291-453/Domain: cytochrome P450 homology <P45>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, submitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thallana chromosome II BAC T9I4 genomic sequence.
A;Reference number: 214710
A;Accession: T02739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable cytochrome P450 At2g29090 [Imported] - Arabidopsis thallana N;Alternate names: cytochrome P450 homolog T914.17 C;Species: Arabidopsis thallana (mouse-ear cress) C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-F C;Accession: T02739; D84692
                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: D84692
                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-482 <STO>
                                                                                                                                                                                                                                                                                                        A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
            Local Similarity
les 153; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RVIQETLRVASILSFTFREAVEDVEYEGYLIPKGWKVLPLFRNIHHSADIFSNPGKFDPS
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            Conservative
                                                                                                                                                                                                                                                  T914.17
                                                                                                                                                                                                                                                                                                     GB:AE002093; NID:g3461849; PIDN:AAC33235.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --VAPKPNTFMPFGNGTHSCPGNELAKLEMSIMIHHLTTKY
                                       22.8%;
29.8%;
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            101;
Score 611; DB 2; Le
Pred. No. 4.5e-32;
"" "" amatches 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-Mar-1999 #text_change 16-Feb-2001
         Indels
            68;
                                                                                                                                                       P450
   Gaps
                                                                                                                                                    homology
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L.; Tallon
C.M.; Vente
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A;Map position: 4COP9-4G3845
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase F;433/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000 C:Accession: C71417 R:Bent, E:; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Di R:Bevan, M.; Bancroft, T.; Bent, E:; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Gi avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B. Nature 391, 485-488, 1998 R:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomene erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; A
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A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis A;Reference number: A71400; MUID:98121113; PMID:9461215
A;Accession: C71417
                                                                                                                                                                                                                                                                                                                                                                 A; Gene: d13695c
                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB: 297338; NID: g2244870; PIDN: CAB10309.1; PID: g2244888
                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-487 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytochrome P450 d13695c - Arabidopsis thaliana N:Contains: oxidoreductase (EC 1.-.-.)
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                                                                                 17 SLLSLLLELILLKRRNRKTRENLPPGKSGWPELGETIGYLKPYTATTLGDFMQQHVSKYG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 DYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRY 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194
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77 -----KIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGI-----LG 121
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                                                    SLFLVKIFHWVYQWRNPKTNGKLPPGSMGFPFIGETFEFFKPHDALQFSTFIKDRVLRFF 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DQPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHL 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IADNIIGVIFAATDTTASVLTWLLKYLHDHPNLLQEVSREQFSIRQKIKKE--NRRISWE 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---IMSAFGDKEEPTTIDVIKLLYQRLERGYNSMPLDLPGTLFHKSMKARIELSEELRKV 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKHIMSMDPGEEE----TEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILKFIERK 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTSFRWEVIGDEEGIQYGPFPVPKKGLPIRVTPI 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IEKRRENGREE-----GGLLGVLLGAKDQKRNGLSDSQ 283
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                                                                                                                                                                                    Similarity
                                                                                                                                                  21.7%; Score 581; DB 1; Length 487; ilarity 27.3%; Pred. No. 4e-30; Conservative 100; Mismatches 205; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -VAPKPYTYMPFGNGVHSCPGSELAKLEMLILLHHL 448
                                                                                                                                                       76;
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C;Date: C;Date: C;Acces: R;Lin, M; Koo Neuss, D Nettile A;Title A;Title A;Refer A;Status: A;Status: A;Cross C;Genet: A;Cross C;Genet: A;Map C;Super C;Super C;Keywo F;432/B; Best I Matche Qy Db Db 13	Db Oy Oy Ob Ob Ob Ob Ob Ob Ob O
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02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 23-Marsion: A84859 8.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C., H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umay, Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frase 402, 761-768, 1999 Sequence and analysis of chromosome 2 of the plant Arabidopsi snce number: A84420; MUID:20083487; PMID:10617197 sion: A84859 sion: A84859 sies: 1-485 <sto></sto>	ADFSSIHLSFFRTSLFGDKAIISMDMELN KWSMLVLVGDMHRDMRSISLNFLSHARLRTILLKE ::::::::::::::::::::::::::::::::::
Feb-2001 Stequence_re : A84859 Kaul, S.; Pomerel Feb-2001 Kaul, S.; Rounsley, S.; White, 761-68, 1999 761-68, 1999 guence and analysis o : number: A84420; MUID : A84859 reliminary type: DNA 1-485 <sto> 'erences: GB:AE002093; 'g42850 ion: 2 ly: Synechocystis cythems; iron; metallop ng site: heme iron (C ch 17; Conservative 1 17; Conservative 1 17; Conservative 1 11; : CIAATISSTLFFFRKKHHRFT DFMQOHVSKYGKIYRSNLFGE: DFVNPRIKHGNIFKTRIMGS: DFVNPRIKHGNIFKTRIMGS: LULPSLISHIFFTRIMGS: DFVNPRIKHGNIFKTRIMGS: DFVNPRIKHGNIFKTRIMGS: LULPSLISHIFFTRIMGS: DFVNPRIKHGNIFKTRIMGS: LULPSLISHIFFTRIMGS: DFVNPRIKHGNIFKTRIMGS: LULPSLISHIFFTRIMGS: DFVNPRIKHGNIFKTRIMGS: LULPSLISHIFFTRIMGS: LULPSLISHIFTRIMGS: LULPSLISHIMBER LULPS</sto>	DFSSIHLSFFRA WSMLTUQDMHH SIRIC SKESHH FTFNLMAKHIM- FTFNLMAKHIM- FTFNLMAKHIM- FTFNLMAKHIM- FTFNLMAKHIM-
N: Reb-2001 **Requence_revision 02=reb-2001 **text_change 23-Maj n: A84859 N: A04859 N: Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umay Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frass, 761-768, 1999 Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frass, 761-768, 1999 Requence and analysis of chromosome 2 of the plant Arabidopsis equence and analysis of chromosome 2 of the plant Arabidopsis enumber: A84420; MUID:20083487; PMID:10617197 n: A04859 preliminary type: DNA 1: 1-485 <sto> 1: 1-485 <stos 1-485="" 1:="" 1:<="" <stos="" dna="" prediminary="" td="" type:=""><td>HHLLLE SRYDED SRYDED STEQII</td></stos></sto></sto></sto></sto></sto></sto></sto></sto>	HHLLLE SRYDED SRYDED STEQII
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n: A84859 n: A84859 n: A84859 n: A84859 n: Monsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.; Wonffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umay Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frase Bequence and analysis of chromosome 2 of the plant Arabidopsi bequence and analysis of chromosome 2 of the plant Arabidopsi ne number: A84420; MUID:20083487; PMID:10617197 n: A84859 preliminary stype: DNA s: 1-485 <sto> ii. 1-485 <sto> iii. 1-485 <sto #status="" (axial="" (cys)="" 1-485="" 107;="" 147;="" 203;="" 28.8%;="" 53;="" 5e-30;="" :="" <sto="" bimilarity="" conservative="" cytochrome="" g="" heme="" iii.="" indels="" iron="" l:="" ligand)="" line="" ling="" llllpsllslllflillkrrnrktrfnlppgksgwpflgetigylkpytat-tl="" metalloprotein="" mismatches="" no.="" p450="" pred.="" predicted="" siren;="" site:="" slr0574;="" synechocystis="" td="" ttch="" ="" <=""><td>ADFSSIHLSFFRTSLFGDKAIISMDMELNLEMAKANSVPGVTKSVIRLEG KWSMLVLVGDMHRDMRSISLNELSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAK SISTEMAKANSVPGVTKSVIRLEG KWSMLVLVGDMHRDMRSISLNELSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAK SISTEMAKHIM-SMDPGEEETEQLKKEVTFMKGVVSAPLILARTYMEEGARNGYLDVKETSS KFTFNLMAKHIM-SMDPGEEETEQLKKEVVTFMKGVVSAPLILLPGTAYHFL SKILIGCLAKKVMGEMEPEAAKELALCWRYFQSGWFFFFLNLPGTGVYKMMKVLFVQYT QSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDL SISTEMAMKLLRKTVLTKRASGEELGEFFNIIFGEMEGE LGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIAR SISTEMAMKLLRKTVLTKRASGEELGEFFNIIFGEMEGE</td></sto></sto></sto>	ADFSSIHLSFFRTSLFGDKAIISMDMELNLEMAKANSVPGVTKSVIRLEG KWSMLVLVGDMHRDMRSISLNELSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAK SISTEMAKANSVPGVTKSVIRLEG KWSMLVLVGDMHRDMRSISLNELSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAK SISTEMAKHIM-SMDPGEEETEQLKKEVTFMKGVVSAPLILARTYMEEGARNGYLDVKETSS KFTFNLMAKHIM-SMDPGEEETEQLKKEVVTFMKGVVSAPLILLPGTAYHFL SKILIGCLAKKVMGEMEPEAAKELALCWRYFQSGWFFFFLNLPGTGVYKMMKVLFVQYT QSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDL SISTEMAMKLLRKTVLTKRASGEELGEFFNIIFGEMEGE LGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIAR SISTEMAMKLLRKTVLTKRASGEELGEFFNIIFGEMEGE
coress) cb-2001 #text_ch ceb-2001 #text_ch n.; Benito, M. T.P.; Benito, M. J.A.; Salzberg, J.A.; Salzberg, le 2 of the plant pMID:10617197 70; PIDN:AAD2172 70; PIDN:AAD2172 70; PIDN:AAD2172 70; PIDN:AAD2172 11gand) #status 15gand) #status 15gand) #status 15gand) #status 15gand) #status 15gand) #status 11gand) #status	// // // // // // // // // // // // //
PIDN:AAD21724.	LEMAKANSY LIFYLDSWG LIFYLDSWG LINLPGTAY LINLPGTAY LINLPGTGY LINLPG
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hange 23-Mar-20 , S.E.; Town, C.D. , S.E.; Unmayam, S.L.; Fraser, S.L.; Fraser, C.D. 24.1; GSPDB:GNO 25.1; Gaps 3YLKPYTAT-TL 64 3YLKPYTAT-TL 6	
23-Mar-2001 Cown, C.D.; Umayam, L Fraser, C.)idopsis tha GSPDB:GN001 GSPDB:GN001 Cted cted 5; P450 homo1 Cted 55; S3; Gaps TAT-TL 64 :: KSNRVF 71 LIGKWS 124 ::	
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C.)	

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Mewes, H.W.;

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hypothetical protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 *sequence_revision 02-Mar-2001 *text_change 31-Mar-2001
C:Accession: H86185
C:Heologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Ritle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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C; Superfamily.
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133; Conservative
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07; Mismatches
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A;Map position: 3
A;Introns: 70/2; 178/3; 229/3; 312/3; 343/3; 346/1; 381/3
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome
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A;Cross-references: EMBL:AL353992; GSPDB:GN00061; ATSP:F14D17.40
A;Experimental source: cultivar Columbia; BAC clone F14D17
C;Genetics:
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A; Accession: T48973
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                                                                                                                                                                                              VINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWR
DDQPFAFPFVDFPNGLPIRVSR
                                                                                                                                                                                                                                                                                                            AGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDYK-KMDFTQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLVGDMHRDMRSISLNFLSHARLRT 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145;
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                                                                                                       WQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAE
                                                                                                                                                                                                                                                                            VTQDTTSKAICLAVKFLLENPKVLAELKKEH-EVILESREDKEGGVTWEEYRHKWTFTN- 342
                                                                                                                                                                                                                                                                                                                                                                                                                                              EDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSN-----LSTEQILDLILSLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLMGIFKAFTFDWFRTSYLISAGKGLYNTLW--ACREGMREIKDIYTMRKTSEEKY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FMKGV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TDKDVNMEILRQENKSFILSYPDGLMKPLGKDSLFLKIGNIHKHIKQITLHLLSSEGLKR
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                                                      WEGKELRAGS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ILLKDVERHTLFVLDSWQQNSIFSAQDEAKKFTFNLMAKHIMSMDPGEEETEQLKKEYVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NPKSNGKLPPGSMGFPIIGETLDFFKPYGFYEISPYLKKKMLRYGPLFRTNILGVKTVVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -VSAPLNLPGTAYHKALQSRATILK--FIERKMEERKLDIKE
                                                   -KTFMVFGTGLRQCAGAEFARLQISVFLHHLVTTYNFSLHQ
                                                                                                                                                                 ---MKSGYTIPAGWIVMIIPSVVHFDPEIYENPFEFNPWR
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511
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Pred. No. 6.6e-30;
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                                                                                                                                                                                                                                                                                                                                                                                       DDFLNTAIEESEKAGELLNENAIITLIFTLSC
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Indels

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Gaps

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379 429 369 284 310 252 P450

homology

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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: B8473
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-489 <STO>
A;Cross references: GB:AE002093; NID:g3831452; PIDN:AAC69934.1; GSPDB:GN00139
C;Genetics:
RESULT 14
D96813
D96813
hypothetical protein T30F21.17 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change
C;Accession: D96813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: At2g32440
A;Map position: 2
C;Superfamily: Synechocystis cytochrome P450 slr0574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: B84733
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| CEVLRYPAAHLPNGISINISK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PYTATTLGDFMQQHVSKYGK--IYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FLSHLRKLTFKVI-MYIFLSSESEHVMDSLEREYTNLNYGVRAMGINLPGFAYHRALKAR
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                                                                                                                                                                                                                                                                                                                                                                     LEMAVFIHHLVLKFNWELAEDDQPFAFPFVDFPNGLP----IRVSRIL 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAK 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAPGQKLTLKETREMYYLSQVIDETLRVITFSLTAFREAKSDVQMDGYIIPKGWKVLTWF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----ATILKFIERKMEERKLDI--KEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGW
                                                                                                                                                                                                                                                                                                    LEISIFLHHFLLKYRVERSNPGCPVMF----LPHNRPKDNCLARITRTM
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Pred. No. 5.9e-28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             -GYTPKAGTFLPFGLGSHLCPGNDLAK
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                                         #text_change 19-Apr-2002
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cytochrome P450 DWARF3 - maize
N; Contains: oxidoreductase (EC 1.-.-.)
C; Species: Zea mays (maize)
C; Date: 10-Sep-1999 #sequence_revision:
C; Accession: T02263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-460 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Devansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AE005173; NID:g4836883; PIDN:AAD30586.1; GSPDB:GN00141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.6%; Score 497.5; DB 2; 26.2%; Pred. No. 9.3e-25; tive 102; Mismatches 205;
                                                                                                                                                                                                                                                                               -GKEMIWGSKTFMAFGYGVRLCVGAEFSRLQMAIFLHHLVAYYD
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.S.; Maiti, R.; Ma
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R;Winkler, R.G.; Helentjaris, T.
Plant Cell 7, 1307-1317, 1995
A;Title: The maize dwarf3 gene encodes a cytochrome P450-mediated
A;Reference number: Z14648; MUID:96004534; PMID:7549486

10-Sep-1999 #text_change

21-Jul-2000

early step

'n

gibbe

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A;Experimental source: strain B73

C;Genetics:
A;Gene: dwarf3
C;Function:
A;Descript:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Description: involved in an early step in gibberellin biosynthesis A;Pathway: gibberellin biosynthesis C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology C;Keywords: oxidoreductase F;325-488/Domain: cytochrome P450 homology <P45>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-519 <WIN>
A;Cross-references: EMBL:U32579; NID:9987266; PIDN:
Search completed: March 30, 2003, 12:07:27 Job time: 51 secs
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                                                                                                                                                                                                            QDE-----RGRHLDDD------EIIDVLVMYLNAGHESSGHITMWATV 342
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                                                                                                                                         RQATRDVFVNGYLIPKGWKVQLWYRSVHMDPQVYPDPTKFDPSRWE-----GHSPRAGTF 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 519;
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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Match
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Gapop 10.0 , Gapext 0.5
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2681
1 MFETEHHTLLPLLL
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   SwissProt_40:*
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   B
            C90C_ARATH
CP95_BRARE
C883_ARATH
CP26_BRARE
C881_MAIZE
C120_SYNY3
CP26_MOUSE
C26A_HUMAN
CP26_CHICK
CP26_CHICK
CP26_CHICK
CP26_AEEL
CYPVA_CAEEL
CYPVA_CAEEL
CYPVA_CAEEL
CP16_MOUSE
CP48_MESAU
CP26_RAT
CP52_RAT
CP53_ARATH
CP51_YEAST
CP51_YEAST
CP51_NOUSE
CP53_HUMAN
CP18_DROUSE
CP33_HUMAN
CP18_DROUSE
CP33_HATH
CP51_TOMAN
CP18_DROUSE
CP33_HATH
CP51_RAT
YRV5_CAEEL
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(without alignments)
559.930 Million cell updates/sec
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Q9m666 arabidopsis
Q43147 lycopersico
O23051 arabidopsis
P79739 brachydanio
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1 arabidopsis
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homo sapien
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SOS

Query Match Best Local Similarity

36.5%; 41.9%;

Score 978.5; DB 1; Length 472; Pred. No. 1.7e-51;

BINDING SEQUENCE

418 472 AA;

418 F 53785 MW;

POTENTIAL.
HEME (BY SIMILARITY).
; 41A73F46D64E343F CRC64;

Transmembrane; Heme; Multigene family

Oxidoreductase; Monooxygenase; TRANSMEM 1 21 P(

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CAA60793.1; CAA60794.1; 7; BAB09663.1; 001128; Cytochrome ; p450; 1. 086; CYTOCHROME_P4 e; MODOOXYGENASE;	ry is Instit ormati inst tateme licen licen	ia; ia; pubMed=933 PubMed=933 A Ramura ta S; sis of Arab sis of Arab 6 Mb regio 0(1997).	ubMed= K., K R., N P., N escue escue ongati	7, Cre 7, Las 9, Las 1 (EC 1 CPD 0 a (Mou antae; olioph cales;	DARD;	5000 5000 5000 5000 5000 5000 5000 500
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Matches

79;

Mismatches

171;

Indels

41;

Gaps

8

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RESULT 2
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C99M66; 023242;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cytochrome P450 90C1 (EC 1.14.-.) (ROTUNDIFOLIA3).

ROT3 OR CYP9OC1 OR AT4G36380 OR C7A10 980 OR F23E13.220.

Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Roside eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G., Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N., Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M., Kreis M., Delseny M., Pulgdomenech P., Watson M., Schmidtheini T., Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
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ROTUNDIFOLIA3 gene of Arabidopsis thaliana
e cytochrome P-450 family that is required
elongation of leaf cells.";
Dev. 12:2381-2391(1998).
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S.-A.,
             B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft Hohelsel J., Zimmermann W., Wedler H., Ridley P.,
McCullagh B.,
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Robben
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24

FLIL-

Matches

186;

Conservative

96;

Score 864; DE Pred. No. 1.36 ; Mismatches

-LPPGKSGWPFLGETIGYL---

56

Indels

78;

Gaps

10

DB 1; .3e-44;

Similarity

32.2%;

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Hacken M., Weltjens I., Voet M., Bastlaens I., Aert R., Defoor E., R. Weltzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M., Prandt A., Peters S., van Staveren M., Dirkse W., R. Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W., R. Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W., R. Hauf J., Koetter P., Braun M., Dirkse W., R. Hauf S., Kempel S., Feldpausch M., Lamberth S., Van den Daele H., R. Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H., R. Berneiser S., Hempel S., Feldpausch M., Gleien J., Villarroel R., De Clercq R., R. Clark L., Doggett J., Hall S., Kay M., Lemaard N., McLay K., Mayes R., R. Clark L., Doggett J., Hall S., Kay M., Lemaard N., McLay K., Mayes R., R. Clark L., Doggett J., Hall S., Kay M., Lemaard N., Loehnert T.-H., Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H., Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H., R. Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A., R. Accard C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A., R. Accard S., Schnidt W., Lecharny A., Aubourg S., R. R. Accard P., Weber N., Vitale D., Liguori R., Piravandi E., R. Schnidt W., Lecharny A., Aubourg S., Torres A., R. Haller R., Schnidt W., Lecharny A., Aubourg S., Torres A., Punchle B., Bent E., Johnson S., Tacon D., Jesse T., R. Gibbons T., Weber N., Vitale D., Haase D., Lemcke K., Mewes H.-W., Stocker S., Bielke C., R. Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S., Bielke C., R. Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S., Shedel P., Cordes M., Abu-Threideh J., R. Accarda P., Bevan M., Wilson R.K., de la Bastide M., Habermann K., R. Abermann K., Falkon J., Fulton E., Malt M., Graves T., Harmon G., Edwards J., R. Abermann C., Fulton E., Martielle P., Courtey L., Cloud J., Abbott A., Scott K., Johnson D., R. Abermann E., Yordan C., Kan M., Pepin K., Hillier L., R. Abermann B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., R. R. Abermann S., Schalfer M., Hameed A., Lodhi M., J
BINDING
CONFLICT
SEQUENCE
                                                                                                                              Oxidoreductase; Monooxygenase; Transmembrane; Endoplasmic reticulum; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bloinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contentites requires a license agreement (See http://www.isb-sib.ch/ar or send an email to license@isb-sib.ch).
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PROSITE; PS00086; CYTO
                                                                                                                                                                                                                                                                    Pfam; PF00067;
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-I- FUNCTION: MIGHT BE INVOLVED IN THE BIOSYNTHESIS OF IMPORTANT FOR THE POLAR ELONGATION OF CELLS DURING-I--
SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic in the subcention of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence and analysis of
                                                                                                                                                                                                                                                             L; AB008097; BAA37167.1; -.
L; AL161589; CAB80304.1; ALT_INIT.
L; Z9708; CAB16850.1; ALT_INIT.
L; Z97141; CAB16819.1; ALT_SEQ.
L; AL022141; CAB168199.1; ALT_SEQ.
erPro; IPR001128; Cytochrome_P450.
m; PF00067; p450; 1.
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TISSUE SPECIFICITY:
SIMILARITY: BELONGS
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TO THE CYTOCHROME P450 FAMILY.
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                                     3Y SIMILARITY).
(IN REF. 2).
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Indels Length

Gaps

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177

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128 58 8

464; 61;

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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Cytochrome P450 85 (EC 1.14.-.-) (Dwarf protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYCES
                                               InterPro; IPR001128; Pfam; PF00067; p450;
                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lycopersicon esculentum (Tomato)
Eukaryota; Viridiplantae; Strept
                                                                                                                                                                                                                                     This
                                                                                                                                                                                                                                                                                        Plant
                                                                                                                                                                                                                                                                                                                                                          STRAIN=CV. GCR758;
MEDLINE=96266705; PubMed=8672892;
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                     EMBL; U54770; AAB17070.1;
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                                                                                                                                                                                                                                                               hop G.J., Harrison K., Jones J.J.G.D.;
e tomato Dwarf gene isolated by heterologous transposon tagging
odes the first member of a new cytochrome P450 family.";
nt Cell 8:959-969(196).
SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                  PR00385;
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                                  P450
               CYTOCHROME_P450;
                                                                  Cytochrome_P450
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             RESULT 4
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STRAIN-cv. Columbia;
MEDLINE-21016719; pubmed-11130712;
Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
Chung M.K., Conn L., Conway A.B., Hansen N.F., Hughes B., Huizar L.,
Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
Kim C.J., Koo H.L., Kremenetkkaia I., Kurtz D.B., Kwan A., Lam B.,
Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oxidoreductase; Monooxygenase; Membrane; Heme.
BINDING 414 414 HEME (BY SIMILARITY).
SEQUENCE 464 AA; 53706 MW; D2B2lAAAB7B14E94 CRC64;
                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998 (Rel. 37, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation updat Cytochrome P450 88A3 (EC 1.14.--). CYP88A3 OR AT1G05160 OR YUP8H12.23.
                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C883_ARATH
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                               NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                              37, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; 1.
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-I- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
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White J.A., Guo Y.-D., Baetz K., Beckett-Jones B., Bonasoro J., Hsu K.E., Dilworth F.J., Jones G., Petkovich M.; "Identification of the retinoic acid-inducible all-trans-retinoic acid hydroxylase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Endoplasmic reticulum BINDING 438 43
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PROSITE; PS00086; CYTOCHROME_P450; 1.
Oxidoreductase; Monooxygenase; Membrane; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U68234; AAC60045.1; -.
ZFIN; ZDB-GENE-990415-44; cyp26.
InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; p450; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostel; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. 271:29922-29927(1996). FUNCTION: PLAYS A KEY ROLE IN RET
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                                                                                                                                                                                 ALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWV
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----PFSLQAMKEAATELLFGGHETTASTATSLVMFLGLNTEVVQKVREE----VQEKVE
                                                         LKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKE
                                                                                                                       GLRAR----NFIHSKIEENIRKKIQDDDNENEQKYKDALQLL----IENSRRSDE----
                                                                                                                                                                                                                                                                                                              IFSAQDEAKKFTFNLMAKHIMSMDPGEEET---EQLKKEYVTFMKGVVSAPLNLPGTAYHK 230
                                                                                                                                                                                                                                                                                                                                                                        ILGSDTLSNVHGVQHKNKKKAIMRAFSRDALEH-----YIPVIQQEVKSAIQEWLQKDS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---LQRRKFLRMKRQKYGCIYKTHLFGNPTVRVMGADNVRQILLGEHKLVSVQWPASVRT 118
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27.6%;
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15-DEC-1998
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                                                                                                                                                                                                              Oxidoreductase;
                                                                                                                                                                                                                                   Pfam; PF00067; p450;
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                                                                                                                                                                                                                                                                                                                                                                                                "The maize Dwarf3 gene encodes a cytochrome P450-mediated early in Gibberellin biosynthesis."; Plant Cell 7:1307-1317(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Espermatophyta; Magnoliophyta; Liliopsida; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DIO-1902 (Rel. 41, Last annotation update)
Cytochrome P450 88A1 (EC 1.14.-.-) (DWARF3 protein).
CYP88A1 OR D3.
                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-cv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAIZE
              187
                                 153
                                                                                                                                                                                                                                                                                                                                                                                                                                     Winkler R.G., Helentjaris T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96004534; PubMed=7549486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-cv. B73;
                                                        129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C881_MAIZE
                                                                           93
                                                                                                69
                                                                                                    36 RFNLPPGKSGWPFLGETIGYLKPYTATTLGDFMQQHVSKYGK--IYRSNLFGEPTI-VSA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                         VEGETATIVE MERISTEM, AND SUSPENSION CULTURE CELLS. SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: Gibberelling TISSUE SPECIFICITY:
       YLPFIDRTVTSSLRAWADHGGSVEFLTELRRWTFKIIVQ-IFLGGADQATTRALERSYTE
                   LLKDVERHTLFVLDSW-QQNSIFSAQDEAKKFTFNLMAKHTMSMDPGEEETEQLKKEYVT
                                               AEGCKQVLMDDDA--FVTGWPKATVALVGPRSFVAMPYDEHRRIRKLTAAPINGFDALTG
                                                                   DAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLVGDMHRDMRSISLNFLSHARLRTI 152
                                                                                        RARLPPGEMGWPLVGGMWAFLRAFKSGKPDAFIASFVRRFGRTGVYRSFMFSSPTVLVTT 128
                                                                                                                                                                                                                                                        U32579; AAC49067.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAKVLLKIFLVELTQHCNWILSNGPPTMKTGPTIYPVDNLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAKLEMAVFIHHLVLKFNWELAEDDQ-----PFAFPFVDFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YSICDTHDVADVFPNKEEFQPERFM-----SKGLEDGSRF--NYIPFGGGSRMCVGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSGSGSFSTWGNNYMPFGGGPRLCAGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGMYTPGKGLSMELLDQLKYTGCVIKETLRINPPVPGGFRVALKTFELNGYQIPKGWNVI
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                                                                                                                                                                                                                           PS00086;
                                                                                                                                                                                                                                             IPR001128;
                                                                                                                                                                                466
519 /
                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                 Gibberellin biosynthesis; early step.
PECIFICITY: EXPRESSED IN ROOTS, DEVELOPING
VE MERISTEM, AND SUSPENSION CULTURE CELLS.
                                                                                                                                                                                AA;
                                                                                                                                                                                                   Monooxygenase;
21 Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                              466 HI
57906 MW;
                                                                                                                                                                                                                        CYTOCHROME_P450; 1.
                                                                                                                                               18.3%; 28.2%;
                                                                                                                                                                                                                                           Cytochrome_P450.
                                                                                                                                      91;
                                                                                                                              Pred. No. 2e-22
91; Mismatches
                                                                                                                                                         Score 491.5;
                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                          HEME (BY
                                                                                                                                                                             EME (BY SIMILARITY).
0F8977A024316D95 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       519
                                                                                                                                                2e-22;
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a; Poales; Poaceae; PACC cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA
                                                                                                                                                        DB 1;
                                                                                                                                     189;
                                                                                                                                                                                                             Heme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         483
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                                                                                                                                    Indels
                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                               LEAVES,
                                                                                                                                                      . 519;
                                                                                                                                    49;
                                                                                                                                 Gaps
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                          211
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                                                                                                                                  11;
    RESULT 7
C120_SYNY3
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                                                      InterPro;
Pfam; PF0(
     SEQUENCE
                                   PROSITE; PS00086; CY1
                      Complete proteome.
                               Hypothetical protein; Oxidoreductase;
                                                                            EMBL; D64003; BAA10496.1;
                                                                                                                                                                                                                                      Tabata S.
                                                                                                                                                                                                                                                                                   MEDLINE-97061201; PubMed-8905231;
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96127529; PubMed=8590279;
Kaneko T., Tanaka A., Sato S., Ko
                                                                                                                                                                                                                                                                                                                                                               Sugiura M., Tabata
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QDE----
                                                               IPR001128; Cytochrome_P450
    444 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                           CYTOCHROME_P450;
 391 H
50578 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RGRHLDDD
                                                                                                                                                                                                                                                                                                                                                                       Sato
             HEME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
8F62A9EED3B54BDC
             (BY
            SIMILARITY)
                             Monooxygenase;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q59990;
Q59990;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative cytochrome P450 120 (EC 1.14.-.-)
CYP120 OR CYP OR SIR0574.
                                                                                                                                                                                                                                                                               "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."
                                                                                                                                                                                                                                                                                                                                                                                               Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nal
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimurr
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Sequence analysis of the genome of the unicellular cyanobacterium synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome."; DNA Res. 2:153-166(1995).
                                                                                                                                                                                                                               DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RQATRDVFVNGYLIPKGWKVQLWYRSVHMDPQVYPDPTKFDPSRWE-----GHSPRAGTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSF
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                                                                                                                                                                                                                                                                                                                                                                                   S., Kimura T.,
S., Okumura S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Miyajima
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RESULT 8
CP26_MOUS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CP26_MOUSE STANDARD; PRT; 497 AA.

055127; 09R1F4;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cytochrome P450 26 (EC 1.4.--) (Retinoic acid-metabolizing cytochrome) (P450RAI) (Retinoic acid 4-hydroxylase).

CYP26AI OR CYP26 OR P450RA.
                                                                                                                                                                                                                                                                                                                     "Metabolic inactivation of retinoic acid by differentially expressed in developing mousemand. 16:4163-4173(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                               MEDLINE-98113212; PubMed-9442090;
Abu-Abed S.S., Beckett B.R., Chiba H., Chithalen J.V., Jones G.,
Metzger D., Chambon P., Petkovich M.;
"Mouse P450RAI (CYP26) expression and retinoic acid-inducible retinoic acid metabolism in F9 cells are regulated by retinoic acid receptor gamma and retinoid X receptor alpha.";
J. Biol. Chem. 273:2409-2415(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                     Fujii H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOUSE
          MEDLINE-20515038;
                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                 Kato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-C3H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97392446; PubMed-9250660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                 S., Hamada H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVERHTLFVLDSWQQNSIFSAQDEAKKFTFNLMAKHIMSMDPGEE--ETEQLKKEYVTFM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQACPKAVEELREEHLEIARAKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFLHR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FLFTKEQETFQATWPLSTRILLGPNALATQMGEIHRSRRKI----LYQAFLPRTLDSYLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGQHSDIRERVRQE-----QNKLQLSQ-ELTAETLKKMPYLDQVLQEVLRLIPPVGGGFR
                                                                                                                                                                                                                                                                                                                                                                                                                     Sato
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          PubMed=11063033
                                                                                                                                                                                                                                                                                                                                                                                                                        Kaneko
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Pred. No. 8.5e-22;
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Sciurognathi; Muridae;
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; Murinae; Mus
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AKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVL
                                                                                                                                                                                                                                                                           AQDEAKKFTFNLMAKHIMSMDPGE----EETEQLKKEYVTFMKGVVSAPLNLPGTAYHKA
                                                                                                                                                  VKARNLIHARIEENIRAKIRRLQATEPDGGCKDALQLLIEHSWE-----
                                                                                                                                                                                                                                               VYPEVKRLMFRIAMRILLGCEPGPAGGGEDEQQLVEAFEEMTRNLFSLPIDVPFSGLYRG
                                                                                                                                                                                                                                                                                                                                                                                         GILGKWSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQ--NSIFS 175
                                                                                               LGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIAR
                                                                                                                                                                                            LQSRATILKFIERKMEE--RKLDIKEED----QEEEEVKTEDEAEMSKSDHVRKQRTDDDL
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-LLFGGHETTASAATSLITYLGLYPHVLQKVREEIKSKGL

406

-RGERLDMQ-

286 236 176

231

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STITIURE REPRESENTATION OF THE PROPERTY OF THE
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"Identification of tuftelin- and amelogenin-interacting proteins using the yeast two-hybrid system.";
Connect. Tissue Res. 38:257-267(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF115769; AAD17217.1;
EMBL; BC012673; AAH12673.1;
HSSP; P14779; 1JPZ.
MGD; MGI:1096359; Cyp26a1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oxidoreductase; Monooxygenase; Membrane; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00067; p450; 1. PRINTS; PR00385; P450.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001128; Cytochrome_P450.
                                                                                                                                                                                     10 LPLLLLPSL----LSLLLFLILLK------RRNRKTRFNLPPGKSGWPFLGETIGYLK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Plays a key role in retinoic acid metabolism. Acts on retinoids, including all-trans-retinoic acid (RA) and its stereolsomer 9-c1s-RA. Capable of both 4-hydroxylation and 18-hydroxylation. Responsible for generation of several hydroxylated forms of RA, including 4-OH-RA, 4-oxo-RA, AND 18-OH-RA. SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum. INDUCTION: BY RETINOIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               European Bioinformatics Institute.
                                                                                                                           LPALLASALCTFVLPLLLFLAALKLWDLYCVSSRDRSCALPLPPGTMGFPFFGETL----
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                                                PYTATTLGDFMQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIG 117
-QMVLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGEHRLVSVHWPASVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y12657; CAA73206.1; -.
                                                                                                                                                                                                                                                         al Similarity
148; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00086;
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                                                                                                                                                                                                                                                      Conservative
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356
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28.4%;
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                                                                                                                                                                                                                                                         78;
                                                                                                                                                                                                                                                  Score 461; DB
Pred. No. 1.2e
78; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                       S -> T (IN REF. 3).
L -> P (IN REF. 4).
I -> T (IN REF. 4).
Y -> H (IN REF. 4).
33B07D7C29134471 CRC64;
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                                                                                                                                                                                                                                                                                DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Microsome;
                                                                                                                                                                                                                                                                                                                Length 497;
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                                                                                                                                                                                                                                                      64;
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RESULT 9
C26A_HUMAN
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the Euro
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G9NR63; Q9NP41;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cytochrome P450 26A2 (EC 1.14.-.-) (P450RAI-2)
                                                                                                                                                                                                                                                                                                                                                                                         White J.A., Ramshaw H., Taimi M., Stangle W., Zhan White J.A., Ramshaw H., Taimi M., Stangle W., Zhan Creighton S., Tam S.-P., Jones G., Petkovich M.; "Identification of the human cytochrome P450, P451 predominantly expressed in the adult cerebellum at all-trans-retinoic acid metabolism."; Proc. Natl. Acad. Sci. U.S.A. 97:6403-6408(2000).
                                                                                                                                        EMBL;
                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        metabolizing cytochrome). CYP26A2 OR P450RAI2.
                                                                          InterPro; IPR001128; Pfam; PF00067; p450; PRINTS; PR00385; P45
                                                                                                                 MIM;
                                                                                                                         EMBL;
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SEQUENCE FROM N.A.
Bauer (
 SEQUENCE
                         BINDING
                                       Endoplasmic
                                              Oxidoreductase; Monooxygenase; Membrane;
                                                            PROSITE;
                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                              entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rissue-Retina;
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                                                                                                                                                                            Buropean Bloinformatics Institute. There are no rest
by non-profit institutions as long as its content
filed and this statement is not removed. Usage by an
ities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                 INDUCTION: By retinoic acids (RA). SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                           cerebellum and pons
                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: Highly expressed in brain,
                                                                                                                                                                                                                                                                                                                      similarity)
                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Membrane-bound.
                                                                                                                                                                                                                                                                                                                                              ENZYME REGULATION: Has a preferred activity towards substrates: all-trans-RA > 9-cis-RA > 13-cis-RA.
                                                                                                                                                                                                                                                                                                                                                                       generation of several hydroxylated forms of RA, 4-oxo-RA, and 18-OH-RA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LCKSNQDNKLDMETLEQLKYIGCVIKETLRLNPPVPGGFRVALKTFELNGYQIPKGWNVI
                                                                                                                605207;
                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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                                                                                                                         AF252297; AAF76003.1;
ACCOCTOCO AAF65576.1;
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                                                            CYTOCHROME_P450;
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57512
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HEME (POTENTIAL).
Q -> QKCTLRETRVWLPQ
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                                                 Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae;
                                                                                                                                                                                                                                                                                                                                  Endoplasmic reticulum
                                                                                                                                                                            http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P450RAI-2,
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15-JUN-2002 (Rel. 41, Last annotation update)
Cytochrome P450 26 (EC 1.14. --) (Retinoic acid degrading CYP26) (XCYP26) (Retinoic acid converting enzyme) (RACE).
CYP26A1 OR CYP26.
          This
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=99077803; PubMed=9857192;
                                                                                                                DEMBO
                                                                                                                                                     Hollemann T.,
                                                                                                                                                                                                                                                        Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                  093323;
                                                                                                                                                                                                                                                                                                                                                                            XENLA
                                                                                                  -!- FUNCTION: Plays a
                                                                                                                                      "Regionalized metabolic
                                                                                                                                                                                                      NCBI_TaxID=8355;
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          SWISS-PROT entry is copyright.
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                                 By retinoic acid.
BELONGS TO THE CYTOCHROME P450 FAMILY.
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Best Local S
Matches 149
                                                                                                                                                                                                                                Q9PUB4; Q9PUG2;
15-JUN-2002 (Rel. 4
15-JUN-2002 (Rel. 4
15-JUN-2002 (Rel. 4
                                                                                                  CYP26A1 OR CYP26.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                        Archosauria; Aves;
                                                                                                                                                                                   CYP26)
                                                                                                                                                                                                        Cytochrome P450
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NCBI_TaxID=9031;
[1]
                                                                                                                                                                                                                                                                                                                                        CP26_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Endoplasmic reticulum.
BINDING 437 437
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PROSITE; PS00086; CYTOCHROME_P450;
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Pfam; PF00067; p450; 1.
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                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                        26
                                                                                                                                                                                                   41, Created)
41, Last sequence update)
41, Last annotation update)
41, Last annotation call
                                                                        Neognathae;
                                                                        Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.6%;
28.7%;
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                                                                        Phasianidae; Phasianinae;
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Best Local Sin
Matches 141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-Embryonic spinal cord;
MEDLINE-20057772; PubMed-10588879;
Swindell E.C., Thaller C., Sockanathan S., Petkovich M., Jessell T.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Plays a key role in retinoic acid metabolism. Appears be involved in the specific inactivation of all-trans-RA.

Responsible for generation of several hydroxylated forms of RA, including 4-OH-RA, 4-OXO-RA, and 18-OH-RA.

-!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.

-!- DEVELOPMENTAL STAGE: EXpressed at stage 4 in the ectoderm, stage 5-7 in the nascent notochord and at stage 7 its expression decreases in the anterior part of the embryo. From stage 7-10 it expression is restricted to the dorsal folds of the neural tube.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complementary domains of retinoic acid production and degradation the early chick embryo."; Dev. Biol. 216:282-296(1999).
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endoplasmic
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230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression in the ectoderm.
INDUCTION: By retinoic acid.
SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and to rhombomere 2. At stage 10, it is expressed in the lateral plate endoderm and in the tail bud and by stage 11/12 it disappears in the neural tube, followed by a confined expression at stage 12 to dorsal neural tube and at stage 15 an increasing
 GLYRGLRAR--
                                                                                                                                                              GKWSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQ---
                                                                                                                                                                                                               ATTLGDFMQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGIL 120
                                                                                                                                                                                                                                                                                              LLPLLLPSLLSLLLFLILLK-----RRNRKTRFNLPPGKSGWPFLGETIGYLKPYT
                            AYHKALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDL
                                                             AGPCLLVYPEVKRLMFRIAMRILLGFQPRQASPDGEQQLVEAFEEMIRNLFSLPIDVPFS
                                                                                            -----DEAKKFTFNLMAKHIMSMDPGE---EETEQLKKEYVTFMKGVVSAPLNLPGT
                                                                                                                               GSGCLSNLHNGQHKHRKKVIMQAFS
                                                                                                                                                                                             VLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGAENVRHILLGEHRLVSVQWPASVRTIL
                                                                                                                                                                                                                                                              LVASALCTFLLPLLLFLAAVRLWDLYCASGRDPSCPLPLPPGTMGLPFFGETL----QM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pro; IPR001128; Cytochrome_P450
PF00067; p450; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF185266; AAD56546.1;
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                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              reticulum.
437 437
371 371
472 474
                                                                                                                                                                                                                                                                                                                                                                                                 492 AA;
                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                               55264 MW;
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26.3%;
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I -> V (IN REF. 2).
GPI -> SPT (IN REF.
W; 7F28B72E75C232FB (
                                                                                                                                                                                                                                                                                                                                              Score 439.5;
Pred. No. 2.:
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RY TISSUE SPECIFICITY.

RY MEDLINE-99045433; PubMed=9826557;
RA Trofimova-Griffin M.E., Juchau M.R.;

RY Trofimova-Griffin M.R.;

RY Trofim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
CP26_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sonneveld E., van den Brink C.E., van der Leede B.M., Schulkes R.K. Petkovich M., van der Burg B., van der Saag P.T.; Petkovich M., van der Burg B., van der Saag P.T.; Phuman retinoic acid (RA) 4-hydroxylase (CYP26) is highly specific "Human retinoic acid (RA) 4-hydroxylase (CYP26) is highly specific all-trans-RA and can be induced through RA receptors in human breas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           White J.A., Beckett-Jones B., Guo Y.-D., Dilworth Jones G., Petkovich M.; Jones G., Petkovich M.; "CDNA cloning of human retinoic acid-metabolizing identifies a novel family of cytochromes P450."; J. Biol. Chem. 272:18538-18541(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cytochrome P450 26 (EC 1.14.--) (Retinoic cytochrome) (P450RAI) (hP450RAI) (Retinoic CYP26AI OR CYP26.
                                                                                                                between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell Growth Differ. 9:629-637(1998).
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MEDLINE-98380037; PubMed-9716180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CP26_HUMAN
043174;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97373542; PubMed=9228017; White J.A., Beckett-Jones B., Guo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606
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                                                                               ween the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    colon carcinoma cells."
                                            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIPFGGGLRSCVGKEFAKVLLKIFTVELARSCDWQLLNGPPTMKTGPIVYPVDNLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Catarrhini; Hominidae,
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(Retinoic acid-metabolizing
(Retinoic acid 4-hydroxylase)
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                                                                                                                                                                                            RESULT
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Best Local Similarity
                                                                                                       01-NOV-1997
01-NOV-1997
30-MAY-2000
Putative cyt
         SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                    Eukaryota; Metazoa;
                                                                              Caenorhabditis elegans.
                                                                                              CYP13A5 OR T10B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an
                                           NCBI_TaxID=6239
                                                           Rhabditidae;
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MIM; 602239; -.
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PROSITE; PS00086; CYTC
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                                                                                                                                                                                                                                                        AGSELAKLEMAVFIHHLVLKFNWELAE----
                                                                                                                                                                                                                                                                                                                            SKGLLCKSNQDNKLDMEILEQLKYIGCVIKETLRLNPPVPGGFRVALKTFELNGYQIPKG
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                                                                                                                                                                                                                                                                               WNVIYSICDTHDVAEIFTNKEEFNPDRFMLPHPEDASRFS
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                                                                                                        cytochrome
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(Rel.)
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                                                        Peloderinae;
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35, Last sequence update)
39, Last annotation updat
me P450 CYP13A5 (EC 1.14.-
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                                                                Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
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27.0%;
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                                                        Caenorhabditis.
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Pred. No. 2.9e-19;
5; Mismatches 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical
BINDING 4
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PROSITE; PS00086; CYTOCHROME_P450;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
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Pfam; PF00067; p450; 1.
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FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED
COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.
SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                    GPRICIGMRLAMMEKKMLLTHILKKYTFE
                                                                                                                         GPRLCAGSELAKLEMAVFIHHLVLKFNWE
                                                                                                                                                                    IPSGWKVLPVISAVHLDNSRY-DQPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGG
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                                                                                                                                                                                                                                                            QRTDDDLLGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELRE
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                                                                                                                                                 IEKGTNVQVDTWTLHYDPKVWGEDANEFRPERWE----
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PROSITE; PS00086; CYTOCHROME_P450; 1.
Hypothetical protein; Oxidoreductase;
BINDING 464 464
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STRAIN-Bristol N2;
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InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; P450; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94
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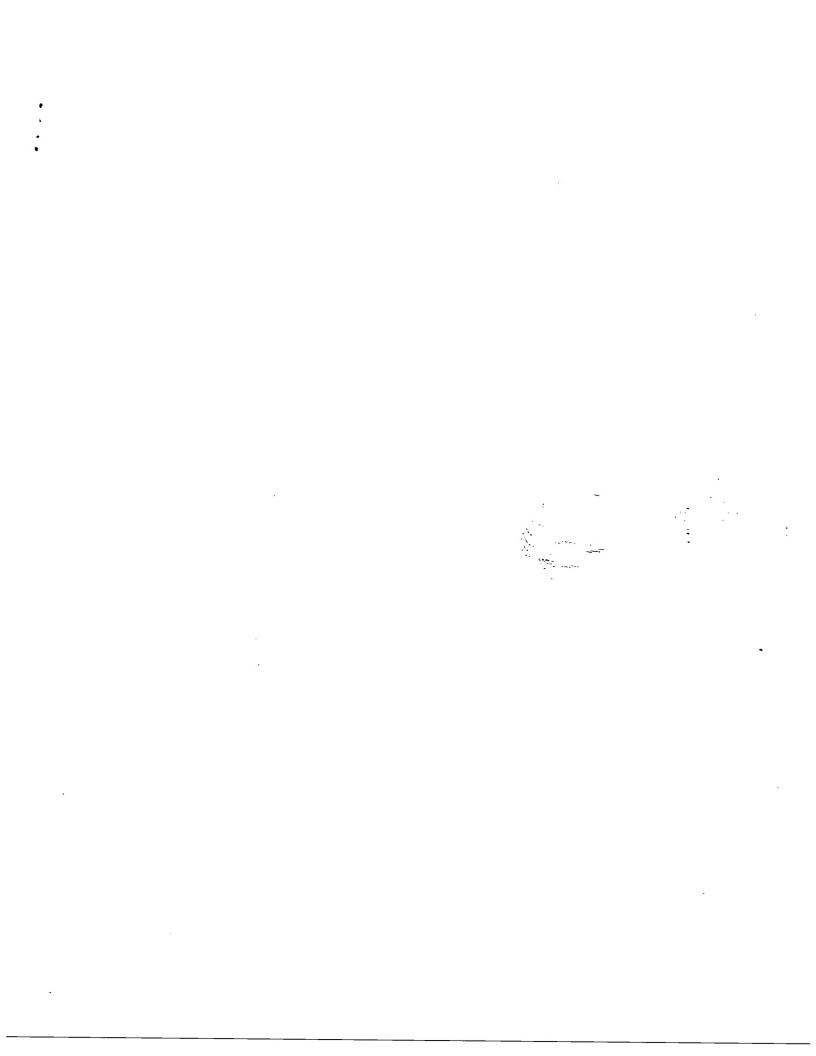
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RA De Keyser A., Buysshaert C., Glelen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
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RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Clefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Percz-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Gibbons T., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Frishman D., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Schon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
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RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Antonoiu B., Zidanic M., Stronge K., Drone K., Drone K.,
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Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche
Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor
Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
Mooljman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
Mooljman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
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Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
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MEDLINE-98281573;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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16-OCT-2001 (Re
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Jham S.-A., McCul
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                        GSFSTWGNNY-----MPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAEDDQ
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                                                      LIPRSPTDDMKIGGYDVPRDTIVMVNAWAIHRDPEIWEEPEKFNPDRY---NDGC----
                                                                                                         ANLLRNPEVLEKARSE-----IDEKIGKDRLIDESDIAVLPYLQNVVSETFRLFPVAPF
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1 MFETEHHTLLPLLLLPSLLSLLLFLILLKRRNRKTRENLPPGKSGWPFLGETIGYLKPYT 60 	Query Match 100.0%; Score 2681; DB 10; Length 513; Best Local Similarity 100.0%; Pred. No. 1.6e-184; Matches 513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Heme; Monooxygenase; Oxidoreductase. SEQUENCE 513 AA; 58867 MW; B1639BDD9A4DA6F3 CRC64;	PÉAN; PEO0067; PÁSO; 1. PROSITE; PS00086; CYTOCHROME_P4SO; UNKNOWN_1.	EMBL; AF044216; AAC05093.1;	-1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.	biosynthesis.";	brassinosteroid	"The DWF4 gene of Arabidopsis encodes a cytochrome P450 that mediates	Feldmann K.A.:	MEDLINE=98158690; PubMed=9490746;	STRAIN=WS-2;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=3702;	eurosids II; Brassicales; Brassicaceae; Arabidopsis.	spermatyora, viituipianidas, sitepopinyda; amuiyopinyda; iidoimeopinyda; Spermatyora, viituipianidas, sitepopinyda; amuiyopinyda; iidoimeopinyda;	Arabiopsis Chailana (Mouse-ear Cress).	DWF4	Steroid 22-alpha-hydroxylase.	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)	(TrEMBLrel 07,	01-AUG-1998 (TremBLrel. 07, Created)	O64989 PRELIMINARY; PRT; 513 AA.	

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  Cheuk H
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          SEQUENCE FROM N.A.
                                                                   Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-MAY-2000 (TrEMBLrel. 13, 1
01-JUN-2002 (TrEMBLrel. 21, 1
Steroid 22-alpha-hydroxylase
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Submitted (NOV-1999)
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Q9LKH7;
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
Cytochrome P450.
CYP90A2.
Vigna radiata.
Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae; Vigna.
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Kawai J., Lam B.
Nguyen M., Onode
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Seki M.,
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NCE 513 AA; 58867 MW; B163
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512; Conservative
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                                                                                                                 PRELIMINARY;
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
[1]
                                                                             Q9FX29 PRELIMINARY; PRT; 512 AA.
Q9FX29;
Q1-MAR-2001 (TIEMBLrel. 16, Created)
Q1-MAR-2001 (TIEMBLrel. 16, Last sequence update)
Q1-MAR-2002 (TIEMBLrel. 20, Last annotation update)
Steroid 22-alpha-hydroxylase, putative.
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InterPro; IPR001128; Cytochrome_P450. Ffam; PF00067; P450; 1.
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PROSITE; PS00086; CYTOCHROME_P450;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                       VPAEEDKLVFFPTTRTQKRYPIIVKR 468
                                                                                                                                                                                                                                ELAEDDQPFAFPFVDFPNGLPIRVSR 511
                                                                                                                                                                                                                                                    LSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDYKKMD
                                                                                                                                                                                                                                                                                                    FTQHVVNETLRVANIIGGIFRRATTDIDIKGYTIPKGWKVFASFRAVHLNPEYYKDARTF
                                                                                                                                                                                                                                                                                                                   FTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLF
                                                                                                                                                                                                                                                                                                                                                   LALLVAGYETTSTIMTLAVKFLTETPLALAQLKEEHDQI-RARSDPG-APLEWTDYKSMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LMAKHIMSMDPGEEETEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILKFIERKM
                                                                                                                                                                                                                                                                                                                                                                                                   EERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVL-KHSNLSTEQILDLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAKKFTFN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FMDERVRRYGSIFMTHVFGEPTVFSADPELNRFILQNEGKLLDCSYPGSISNLLGKHSLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monooxygenase; Oxidoreductase.
NCE 474 AA; 54037 MW; A2542A809C5BAC6D CRC64;
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40.1%;
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Pred. No. 3e-60;
7; Mismatches 1
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Best Local S
Matches 181
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01-DEC-2001
01-JUN-2002
CYP90D.
                                                     Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                             NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.; Frabidopsis thaliana chromosome 1 BAC T9124 genomic sequence."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AC012396; AAG30983.1; -.
InterPro; IPRO01128; Cytochrome_P450.
PFam; PF00067; p450; 1.
PRINTS; PR00085; P450.
PROSITE; PR00085; P450.
PROSITE; PR00085; P450.
PROSITE; PR00085; P450.
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Pred. No. 4.2e-54;
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Matches 176
    Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A., Ecker J.R.;
                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
MCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                  Q9LN73;
01-OCT-2000 (TIEMBLIEL: 15,
01-OCT-2000 (TIEMBLIEL: 15,
01-JUN-2002 (TIEMBLIEL: 21,
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AB066286; BAB62109.1;
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR00504; RNA_rec_mot.
Pfam; PF00067; p450; 1.
PROSITE: PS00086; CYTOCHROME_P450; UNKNOWN_1.
PROSITE: PS00030; RRM_RNP_1; UNKNOWN_1.
Heme; Monooxygenase; Oxidoreductase.
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Pred. No. 1.
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01-OCT-2000 (TrEMBLrel. 15, C:
01-OCT-2000 (TrEMBLrel. 25, L:
01-MAR-2002 (TrEMBLrel. 20, L:
Hypothetical 43.9 kDa protein
F18022_190.
Bevan M., Murphy G., Rudd S., Lemcke K., M
Submitted (APR-2000) (2)
                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                SEQUENCE FROM
                                                                                                                     NCBI_TaxID=3702;
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EMBL/GenBank/DDBJ databases

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eudicots; Rosidae;

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Last sequence update)

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Last annotation

update)

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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AC025417; AAF88087.1; -
InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; p450; 2.
PRINTS; PR00085; P450; 2.
PRINTS; PR00086; CYTOCHROME_P450; UNKNOWN_1.
Heme; Monooxygenase; Oxidoreductase.
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                                                                                                CVINETLRLGNVVRFLHRKALKDVRYK------GYDIPSGWKVLPVISAVHLDNSRYDQP
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                                    FNWELAEDDQPFAFPFVDFPNGLPIRVSR
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RCE 478 AA; 55058 MW; F67A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.7%;
                                                                             -GSKVTNASKHFMAFGGGMRFCVGTDFTKLQMAAFLHSLVTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 822; DB 10;
Pred. No. 5.6e-51;
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475
                                      511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
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                                                                                                                  482
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Best Local
                                       "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, clone:P0419B01.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL, AP003244; BAB56089.1;
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                                                                                                                                                                                                                                                                                                 Oryza sativa (Rice).
Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                      094IW5 PRELIMINARY; PRT; 490 AA.
094IW5; PTELIMINARY; PRT; 490 AA.
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Cytochrome 4500-like protein.
P0419B01.5.
                                                                                                                                                                        STRAIN-CV. NIPPONBARI
Sasaki T., Matsumoto
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; p450; 1.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
Heme; Hypothetical protein; Monooxygenase; Oxidoreductase.
SEQUENCE 382 AA; 43889 MW; 1BC5685AB73B4E30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EU Arabidopsis sequencing project;
Submitted (APR-2000) to the EMBL/GenBank/D-
--- SIMILARITY: BELONGS TO THE CYTOCHROME
EMBL; AL163817; CAB87779.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
EU Arabidopsis sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLPVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SELAKLEMAVFIHHLVLKFNWELAEDDQPFAFPFVDFPNGLPIRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLLGWYLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGYTNAIKVRSNRNIHQNAIIEDMNNAIREEDFLDSIISNED------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRLFECSYPRSIGGILGKWSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFV 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GWPFIGETISFFKPHRSDSIGTFLQQRVSRYGKVFKSNICGGKAVVSCDQELNMFILQNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GWPELGETIGYLKPYTATTLGDFMQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNE 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VFPIFTAVHLDPSLHENPFEFNPMRWTKTT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKSWKNCREVEFHKEVKIFTLSVMVNQLLSIKPEDPARLYVLQDFLSYMKGFISLPIPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDSWQQNSIFSAQDEAKKFTFNLMAKHIMSMDPGEEETEQLKKEYVTFMKGVVSAPLNLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKLFTSDYPKAMHDILGKYSLLLATGEIHRKLKNVIISFINLTKSKPDFLHCAENLSISI 121
PF00067; p450; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.4%; Score 815; DB 10; 34.2%; Pred. No. 1.3e-50; Live 87; Mismatches 127;
                                                                                                                                                                   Yamamoto
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                                                                                                                                           genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
on update)
                                                                                                                                         chromosome 1,
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                                                                                                                                                                                                                                                                                                                                         Tracheophyta;
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Best Local
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   460
                        485
                                             412
                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
Heme; Monooxygenase; Oxidoreductase.
SEQUENCE 490 AA; 54824 MW; 9EC2853BBAFBB8
                                                                 425
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                                                                                                           365
                                                                                                                                293
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                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
            WELAEDDQPFAFPFVDFPNGLPIRVS
W-VAEEDHIVNFPTVRLKRGMPIRVT
                                       FNPWRWQQQNNGASSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFN
                                                                               SFTQHVITETLRLGNIIGGIMRKAVRDVEVKGHLIPKGWCVFVYFRSVHLDDTLYDEPYK
                                                                                                                          MIDLMIPAEDSVPVLITLAVKFLSECPLALHQLEEENIQLKRRKTDMGET-LQWTDYMSL
                                                                                           -----LDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSNLSTEQILDL
                                                                                                                                                                                                            AG-EEMQQLKQQFQEFIYGLMSLPIKLPGTRLYRSLQAKKKMARLIQRIIREKRARRAAA
                                                                                                                                                                                                                        PGEEETEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILKFIERKMEERK-----
                                                                                                                                                                                                                                                      HGLVGAFFKSSHLKSQLTADMRRRLSPALSSFPDSSLLHVQHLAKSVVFEILVRGLIGLE
                                                                                                                                                                                                                                                                                                                                                              LLKRRNR-----KTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDFMQQHVSKYGK 77
                                                                                                                                                                       SPPRDAIDVLIGDGSDE-----
                                                                                                                                                                                                                                                                          RSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAKKFTFNLMAKHIMSMD
                                                                                                                                                                                                                                                                                              AVFRSHLFGSATVVTADAEVSRFVLQSDARAFVPWYPRSLTELMGKSSILLINGALQRRV
                                                                                                                                                                                                                                                                                                            LLRRRRRGAGSGKGDAAAAARLPPGSFGWPVVGETLEFVSCAYSPRPEAFVDKRRKLHGS
                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                54824 MW;
                                                                                                                                                                                                                                                                                                                                                                                                 30.3%;
                                                                                                                                                                                                                                                                                                                                                                                        106;
                                                                                                                                                                                                                                                                                                                                                                                                Score 813.5; DB |
Pred. No. 2.4e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                               9EC2853BBAFBB88F CRC64;
 484
                    510
                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          DB 10;
                                                                                                                                                                                                                                                                                                                                                                                     156;
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                                                                                                                                                                                                                                                                                                                                                                                    71;
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                       459
                                                           484
                                                                                411
                                                                                                    424
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RESULT
Q9LIC5
Nakamura Y.;

Nakamura Y.;

"Structural analysis of Arabidopsis Sequence features of the regions of TAC and BAC clones.";

DNA Res. 7:217-221(2000).
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01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-CCT-2000 (TrEMBLrel. 21, Last annotation update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Cytochrome P450-11ke protein.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-COLUMBIA;
                                                                                                                      MEDLINE=20363099;
                                                                                                                                        STRAIN=COLUMBIA;
                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                 Submitted (MAR-2000)
                                                                                                                                                                                                                     Kaneko T.,
                                                                                                                                                                                                                                                                                             NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9LIC5
                                                                                                                                                                                                                   Kato T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                  PubMed=10907853;
                                                                                                                                                                                                               Sato
                                                                                                                                                                                           iato S., Nakamura Y., Asan
to the EMBL/GenBank/DDBJ
  CYTOCHROME P450 FAMILY
                                                          thaliana c 4,251,695
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                                                                                                                                                                                           Asamizu E., T
DDBJ databases
                                                      chromosome
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                                                                                                                                                                                                                                                                                                                                            Tracheophyta;
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RESULT 10
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DT 01-MA
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DE SU32H
ON SOIGH
OC EDUKART
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Best Local S
Matches 163
STRAIN-CV. BTX623;
STRAIN-CV. Young S., Kovchok S., Messignated V., Young S., Kovchok S., Messignated V., Young S., Kovchok S., Messignated V., Apart Strain                                                                                                                                                                                                                                                                                                                                                                                                      SB32H17.4.

Sorghum bicolor (Sorghum) (Sorghum vulgare).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;

Panicoldeae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OBWOR4;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last seque
01-JUN-2002 (TrEMBLrel. 21, Last annot
Putative cytochrome P450-like protein.
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-CV. BTX623; Park Y.-J., Ramakr
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InterPro; IPR0011128; Cytochrome_P450.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PP00067; P450; 1.
PRINTS; PR000385; P450.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
Heme; Monooxygenase; Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8W0R4
                                                                                                                                                                                                                                        Park Y.-J., Ramakrishna
Submitted (JAN-2002) to
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                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4558;
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YVIPKGWCFLAYLRSVHLDKLYYESPYKFNPWRWQERDMNTSS-----FSPFG
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Last annotation update)
                                                                                    S., Messing J.;
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                        SanMiguel P., Emberton J., EMBL/GenBank/DDBJ database
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Matches 170; Conserv
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Q9FMA5;
01-MAR-2001 (TTEMBLTel. 1
01-MAR-2001 (TTEMBLTEL 1
01-MAR-2002 (TTEMBLTEL 2
                                                                                             SEQUENCE SERVINCE MEDITINE-98290546; Pubmed-9628582; MEDLINE-98290546; Pubmed-9628582; Kaneko T., Kotani H., Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00067; p450; l.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1
SEQUENCE 481 AA; 54984 MW; 6145CFFFCOFFT
SEQUENCE FROM N.A STRAIN-COLUMBIA; MEDLINE-21295570;
                                               "Structural analysis of Arabidopsis thaliana chrosequence features of the regions of 1,456,315 bp physically assigned P1 and TAC clones."; DNA Res. 5:41-54(1998).
                                                                                                                                                             NCBI_TaxID=3702;
                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 FNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSNLSTEQI-LDL::||: : : | ::: : | |::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLMAKHIMSMDPGEEETEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILKFIERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAKKFTF 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LPSLLSLLLFLILLK-------RRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLG
                                                                                                                                                                                                                                                                                                                                                                   WKALSKGTMMLYPGLRFPDGFHIQLHK
                                                                                                                                                                                                                                                                                                                                                                                          WELAEDDQPFAFPFVDFPNGLPIRVSR
                                                                                                                                                                                                                                                                                                                                                                                                                 FNPWRWKDTPEPVGGS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAALSVTLLGAILLRWAFKWMNYGRTGGEEGMLLPPGSRGLPFLGETLEFFAASPTLELV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFFKRRLERFGPIFRTNIVGEDMIVSLDPELNARVLQQEERGFQIWYPSSFMRILGADNM
                                                                                                                                                                                                                                           1 (TYEMBLIFE). 16, Created)
1 (TYEMBLIFE). 16, Last sequence upo
2 (TYEMBLIFE). 20, Last annotation upo
P450 (Brassinosteroid-6-oxidase).
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                          N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----NGAERKTVDFFDL------VIDELDKPNSIMSESIALNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 756.5;
Pred. No. 2.9
                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                 KDFMAFGGGLRLCVGAEFAKLQMAMFLHYLVTNYR 452
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                                                                                                                                                                                                                                                        annotation update)
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                                                                                                            Asamizu
                                                                                    chromosome
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                                                                         nineteen
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Best Local S
Matches 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shimada Y., Fujioka S., Miyauchi N., Kushiro M., Takatsuto S., Nomura T., Yokota T., Kamiya Y., Bishop G., Yoshida S.; "Brassinosteroid-6-oxidases from Arabidopsis and tomato catalyze multiple C-6 oxidations in brassinosteroid biosynthesis."; Plant Physiol. 126:770-779(2001).

"I SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY. EMBL; AB009048; BAB08653.1; -.
EMBL; AB095868; BAB60858.1; -.
EMBL; AB035868; BAB60858.1; -.
InterPro; IPR00118; Cytochrome_P450.
Pfam; PF00067; P450; 1.
PRINTS; P800086; CYTOCHROME_P450; UNKNOWN_1.
                Cheuk R., Chen H.,
                           SEQUENCE FROM N.A.
                                                   NCBI_TaxID=3702;
                                                                                                                                                                                                                                     430
                                                                                                                                                                                                                                                                                   381
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                                                                                                                                                                                                                                                                                            SRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGDRLCAGSBLAKLEMAVFI 476
                                                                                                                                                                                                                                                                                                                           GLEDVKSMKFTRAVIYETSRLATIVNGVLRKTTRDLEINGYLIPKGWRIYVYTREINYDA
                                                                                                                                                                                                                                                                                                                                          HHLVLKFNWELAEDDQPFAFPFVDFPNGLPIRVS
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                                                                                                                                                                                                                                                                                                                                                                                      FIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSN----L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166;
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NCE 465 AA; 53767 MW; 0C00
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      Carninci
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Kim C.J., Koesema E., Meyers M.C., i P., Dale J.M., Goldsmith A.D., Ha
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32.3%; Pre
ative 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53767 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -EEFKTAFFKLVVGTLSVPIDLPGTNYRCGIQARNNIDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 726; DB 10;
Pred. No. 4.3e-44;
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                                                                     Embryophyta;
edons; core e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                        -TFTDMLGYLMKKEGNRYPL
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 Hayashizaki Y.,
                                                                        eudicots;
                                                                                Tracheophyta;
            Banh J
                                                                      Rosidae;
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RA Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Miranda M., Narussaka M., Nugyen M., Onodera C.S.,
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis ORF clones.",
RT "Arabidopsis ORF clones.",
RT "Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
DR EMBL; AY053728; AAR96559.1; -
DR EMBL; AY053728; AAR36078.1; -
DR EMBL; AY053728; AAR36078.1; -
DR Ffam; PP00067; p450; 1.
DR Pfam; PP00067; p450; 1.
DR Pfam; PP00068; CYTOCHROME_P450; UNKNOWN_1.
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Best Local &
Matches 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00086; CLICCONTROLLER PS000808; Oxidoreductase Heme; Monooxygenase; Oxidoreductase SFOUENCE 465 AA; 53814 MW; 280A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IShida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai Yamadu M., Seki M., Southwick A., Tang C.C., Torlumi M., Yamada K., Yamadaura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                          437
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                                                                                       RWEENGEDKLMVFPRVSAPKGYHLKCS
                                                                                                                     NWELAEDDQPFAFPFVDFPNGLPIRVS
                                                                                                                                                                   LENPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLYLKF
                                                                                                                                                                                                                                       MDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPN 423
                                                                                                                                                                                                                                                                      LVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAKKFTFNL
                                                                                                                                                                                                              MKFTRAVIFETSRLATIVNGVLRKTTHDLELNGYLIPKGWRIYVYTREINYDTSLYEDPM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               VHGPSHRLMRGSLLSLISPTMMKDHLLPKIDDFMRNYLCGWDDLETVDIQEKTKHMAF-L
                                                                                                                                                      IFNPWRWMEKSLESKS --
                                                                                                                                                                                                                                                                                                                                                                ERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSN----LSTEQILD
                                                                                                                                                                                                                                                                                                                                                                                                 SSLLQIAETLKKPEVEEYRTEFFKLVVGTLSVPIDIPGTNYRSGVQARNNIDRLLTELMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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32.1%;
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; Mismatches
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Pred. No. 4.3e-43;
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Q9LH81;

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Best Local Sim
Matches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence features of the regions of 4,251,695 by TAC and BAC clones.";
DNA Res. 7:217-221(2000).
-1 SIMILARITY: BELONGS TO THE CYTOCHROME P450 EMBL; AP002060; BAB02270.1; -
InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450; 1.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
Heme; Monooxygenase; Oxidoreductase.
SEQUENCE 465 AA; 53862 MW; 630A21D0765E0D0D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-COLUMBIA;
Kaneko T., Kato T.,
Submitted (MAY-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
Cytochrome P450.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20363099;
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437
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                                                                                                                                                                                                                                                                                                                                                                                                                      LVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAKKFTFNL 187
                                                                                                                                                                                                              LILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDYKK 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLPSLLSLLLFLILL-----KRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDF
                           NWELAEDDQPFAFPFVDFPNGLPIRVS
                                                                                                                                                                                                                                                                                                                          SSLLQIAETLKKPEVEEYRTEFFKLVVGTLSVPIDIPGTNYRSGFQARNNIDRLLTELMQ
                                                                                                                                                                                                                                                                                                                                                        MAKHIMSMDPGEEETEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILKFIERKME 247
                                                                                                                                                                                                                                                                                                                                                                                           VHGPSHRLMRGSLLSLISPTMMKDHLLPKIDDFMRNYLCGWDDLETVDIQEKTKHMAF-L
                                                                                          LENPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKF
                                                                                                                            MKFTRAVIFETSRLATIVNGVLRKTTHDLELNGYLIPKGWRIYVYTREINYDTSLYEDPM
                                                                                                                                                           MDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPN
                                                                                                                                                                                             QVVTILYSGYETVSTTSMMALKYLHDHPKALEELRREHLAIRERKRP--DEPLTLDDIKS
                                                                                                                                                                                                                                                                                         ERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSN----LSTEQILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKNQRLRYGSFFKSHILGCPTIVSMDAELNRYILMNESKGLVAGYPQSMLDILGTCNIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMMILGLLVIIVCLCTALLRWNQMRYSKKGLPPGTMGWPIFGETTEFLKQGP-----DF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sato S., Nakamura Y., Asamizu E., Tabata ) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.5%;
32.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of Arabidopsis thaliana chromosome 3. the regions of 4,251,695 bp covered b
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Last sequ
Last anno
                                                             ----YFLLFGGGVRLCPGKELGISEVSSFLHYFVTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 711; DB 10;
Pred. No. 5.1e-43;
3; Mismatches 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         630A21D0765E0D0D CRC64;
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                                                                                                                                                                                                                                                            -DMLGYLMKKEDNRYLLTDKEIRD
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Q949P1;
01-DEC-2001
01-DEC-2001
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SEQUENCE FROM N.A.

Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,

Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,

Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,

Tang C., Toriumi M., Yamamura Hayashizaki Y., Ishida J., Jones T.,

Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,

Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B.,

Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B.,
                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001128; Cytochrome_P450
Pfam; PF00067; p450; 1.
PROSITE; PS00086; CYTOCHROME_P450; UN-
Heme; Monooxygenase; Oxidoreductase.
SEQUENCE 467 AA; 53037 MW; 2F4230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E. Shinozaki K., Davis R.W., Ecker J.R., Theologis A.; "Full Length cDNA of gene AT4019230 (GI:7268718)."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

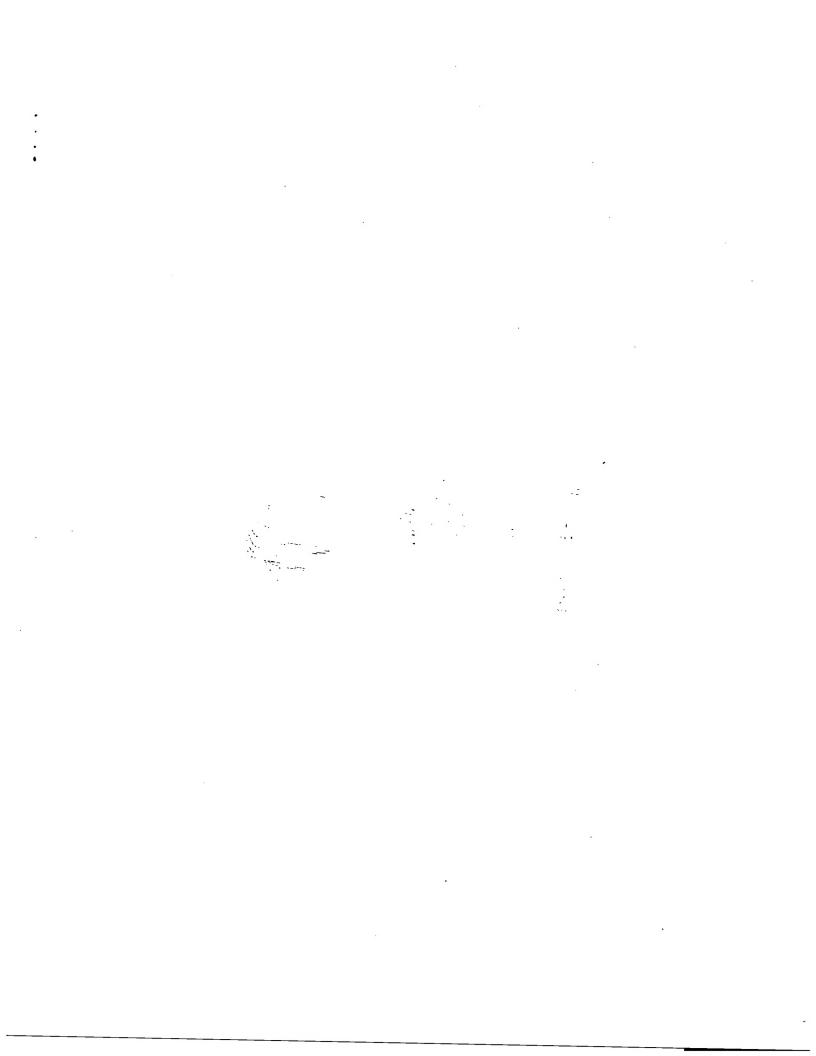
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TremBirel. 19, Created)
01-DEC-2001 (TremBirel. 19, Last sequence update)
01-DEC-2002 (TremBirel. 2), Last annotation update
Putative cytochrome P450 protein.
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                 309
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                                                                                                                                                                                                                                                                                      LLLPSLLSLLLFLILLKRRNRKTRENLPPGKSGWPFLGETIGYLKPYTATTLGDFWQQHV 72
KRYGSVEKTHVLGCPCVMISSPEAAKEVLVTKSHLFKPTEPASKERMLGKQAIFEHQGDY 125
                                             R--
                                                              MSMDPGEEET---EQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILKFIERKMEER
                                                                                                                                                           HAKLRKLVLRAFMPESIRN-MVPDIESIAQDSLRSW-EGTMINTYQEMKTYTFNVALLSI 183
                                                                                                                                                                                    HRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAKKFTFNLMAKHI 192
                                                                                                                                                                                                                                            SKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLVGDM 132
                                                                                                                                                                                                                                                                       LFAGSLFLYFLRCLISQRRFGSSKLPLPPGTMGWPYVGET---FQLYSQDP-NVFFQSKQ
                                                                                                                                                                                                                                                                                                                                 164;
                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                   -GKDEVLYREDLKRCYYILEKGYNSMPVNLPGTLFHKSMKARKELSQILARILSER
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                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOCHROME_P450; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                              25.1%;
                                            -QNGSSH---
                                                                                                                                                                                                                                                                                                                                 96;
                                                                                                                                                                                                                                                                                                                               Score 672.5;
Pred. No. 3e-4
)6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        2F4230446536D955 CRC64;
                                          ----NDLLGSFMGDKEELTDEQIADNIIGV
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                                                                                                                                                                                                                                                              "Arabidopsis cDNA clones.";
Submitted (NOY-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AB020744; BAB10255.1;
-- EMBL; AY065065; AAL57698.1;
-- InterPro; IPR001128; CYTOCHROME_P450.
Pfam; PF00067; p450; 1
PRINTS; PR00086; CYTOCHROME_P450; UNKNOWN_1.

PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                             Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou N
Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9FH76 PRELIMINARY; PRT; 463 AA.
Q9FH76;
Q9FH76;
01-MAR-2001 (TrEMBLrel. 16, Croated)
01-MAR-2001 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Cytochrome P450 (AT5945340/K9EJ5_12).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
129 VGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAKKFTFNLM 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-COLUMBIA;
MEDLINE-20181125; PubMed~10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty P1 and TAC clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Res. 7:31-63(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                 69
                                                                                                                             14 LLPSLLSLLLFLILLK-----RRNRKTRENLPPGKSGWPELGETIGYLKPYTATTLGDFM 68
                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       438
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                               AAKQRRYGSVFKTHVLGCPCVMISSPEAAKFVLVTKSHLFKPTFPASKERMLGKQAIFFH 121
                                                             QQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVL 128
                                                                                               LFLTLSAAALFLCLLRFIAGVRRSSSTKLPLPPGTMGYPYVGET----FQLYSQDP-NVFF
                                                                                                                                                                                                                                       Monooxygenase; Oxidoreductase.
NCE 463 AA; 52366 MW; CCD17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -AEDD---QPFAFPFVDFPNGLPIRVSR 511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GASDGIQYGPFALP----QNGLPIVLAR 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RWQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWEL- 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RVIQETLRVASILSFTFREAVEDVEYEGYLIPKGWKVLPLFRNIHHSADIFSNPGKFDPS 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IFAARDTTASVMSWILKYLAENPNVLEAVTEEQMAI-RKDKEEGES-LTWGDTKKMPLTS
                                                                                                                                                                                            Similarity
                                                                                                                                                                            Conservative
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                                                                                                                                                                    24.5%; Score 658; DB 10;
31.8%; Pred. No. 3.3e-39;
tive 95; Mismatches 184;
                                                                                                                                                                                                                                   CCD17293F553F812 CRC64;
                                                                                                                                                                     184;
                                                                                                                                                                                                   Length 463;
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                                                              425 FNPWRWQQQNNGASSSGSGSFSTWGNNYMDFGGGGRRLCAGSELAKLEMAVFIHHLVLKFN 484
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                                                                                                                                                                     269
                                                                                                                                           365
                                                                                                                                                                                               305
                                                                                                                                                                                                                          236
                                                                                                                                                                                                                                       246 MEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLK-HSNLSTEQILDL
                                                                                                                                                                                                                                                                180 LISIL----GKDEVYYREDLKRCYYILEKGYNSMPINLPGTLFHKAMKARKELAQILANI 235
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WSIVGPSDGIQYGPFALP----QNGLPIALER 461
                   WELAEDDQ-----PFAFPFVDFPNGLPIRVSR 511
                                                FDPSRFE-----VAPKPNTFMPFGSGIHSCPGNELAKLEISVLIHHLTTKYR 433
                                                                                                   PLTYRVIQETLRAATILSFTFREAVEDVEYEGYLIPKGWKVLPLFRNIHHNADIFSDPGK 386
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Search completed: March 30, 2003, 12:06:27 Job time: 66 secs



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SUMMARIES

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GWPFLGETIGYLKPYTATTLGDFMQOHYSKYGKIYRSNLFGEPTIVSADAGLNRFIIQ
NEGRLFECSYPRSIGGIIGKULVGDMHRDMRSISLFLSHARLFTILKOVERH
TLFVLDSWQQNSIFSAQDEAKKFTFNLMAKHINSMDFGEEETEQLKKEYYTFKKGVYS
APLNLFGTAYHKALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDH
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/protein_id="AAC05093.1"
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| 12562...2654,2746...2824,2931...3040,3795...4040)
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/note="member of the cytochrome P450 superfamil:
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Arabidopsis thaliana
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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 84196)
Bloecker, H., Mewes, H.W., Lemcke, K., Mayer, K.F.X., Quetier, F. and

Arabidopsis thaliana.

AL132979.2

Arabidopsis thaliana DNA chromosome AL132979 GI:6782244

84196 bp

DNA 3, BAC

linear Pl clone T3A5

PLN 26-JAN-2000

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On Jan 27, 2000 this sequence version replaced gi:6434247.
Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at; http://www.mips.biochem.mpg.de/proj/thal/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (25-JAN-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail Lemckedmips.biochem.mpg.de,mayerdmips.biochem.mpg.de Project Coordinator: Marcel Salanoubat and Francis Quetier, Groupement d'Interet Public, Centre National de Sequencage - GENOSCOPE; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d'Interet Public, Centre National de Sequencage - Gaston Cremieux, BP191, 91006 Evry Cedex, France;
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EU Arabidopsis sequencing, project.
Direct Submission
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variety="Columbia"
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MPSADPARSYNDYSMIPADEIFIKKRIIPKETSHVHRTIGEELLTEEEGSWYDGNTF
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SLRPILLSSSSETIKGTWRELIGIKRTHVRSKKTDKVNEEVLSODHKIISGNVATREC
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// protest-"die-"cah62435.1"

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VKRGYDDPSGWYLPYSAVHLDNSKTDOHUNKSSUGGESTWGNA
VKRGYDDPSGWYLPYSAVHLDNSKTDOHUNKSSUGAGASSSGGSSSSTSTWGN
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GGTTTGACTGTCCAGTTCGGTAATAATCTAATAACTCTGTCTTTGACCGCACGCTCGTGT
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'gene"TjA5.50"

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                                                                                                                                         GAAGCTCATTGGTTA-GTTTAAGCTTAATAAGAAGATTTTATTAAATTTTTAATGACGATG
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                                                              GAAGCTCATTGGTTAGGTTTAAGCTTAATAAGAAGATTTTATTAAATTTTAATGACGATG
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PUBMED REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 3 AF273674 LOCUS DEFINITION JOURNAL MEDLINÇ 2 (bases 1 to 4629)
Li,J., Maga,J.A., Cermakian,N.,
Direct Submission Plasmodium falciparum Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. 1 (bases 1 to 4629)
Li,J., Maga,J.A., Cermakian,N., Cedergren,R. and Feagin,J.E. Identification and Characterization of a Plasmodium falciparum polymerase gene with similarity to mitochondrial RNA polymerase; Mol. Biochem. Parasitol. 113 (2), 261-269 (2001) AF273674 AF273674 4629 bp DNA linear INV 24-APR-2001 Plasmodium falciparum DNA-dependent RNA polymerase (TRNAP) gene, complete cds; nuclear gene for probable mitochondrial product. Plasmodium AF273674.1 GI:9857984 falciparum Cedergren, R. and

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                                    GCTCAAAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAATTGGG
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NMLIENAKMDVDINVAKNEFKNEYKYYLFLHKTAKNNAEDLYEECKYKKELNYQKFYE
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/db_xref-"taxon:5833"
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<70. .>4581
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/db_xref="GI:9857985"
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GQDQAHHHHHHHHHQLQPQQPQGTVANPPSNEPVRKTQVFREARPGGFRAYEEKYES
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DEDEEGKEALAIKDKLPGGLDEYQNQLYGICNETCTTGGPAALDYVPADAPNGYAYGG
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SKKTNEENKNKEKTNNSKSDGSKAHEKKENETKNTAGENKKVDSTSADNKSTNAATPG
SKKTNCHGGKKTDKTGASTNAATNKGQCAAEGATKGASTSKEATKEASTSKEATKE
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complement(7684. .8322)
/gene="PFB0105c"
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/gene="PFB0100c"
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/gene="PFB0100c"
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/db_xref="GI:3845096"
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/gene="PFB0105c"
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/protein_id="AAC71810.1"
/db_xref="GI:3845095"
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/chromosome="2"
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translation="MKGSGSEKNVYLSNKNKEINMNQQSDNKMCDECDDMNQPGDVNK/
                                                                                                                                                                       /note="predicted by GlimmerM"
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ODS predictions from GeneID may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis (http://genome.imb-jena.de/dictyostelium/) and the Univerity Colonge, Institute for Biochemistry I (http://www.uni-koeln.de/dictyostelium/project.shtml
                                                                                                                                                                                                                                                        Direct Submission
Direct Submission
Submitted (06-APR-2002) Genome Analysis, Institute of Molecular Submitted (06-APR-2002) Genome Analysis, Institute of Molecular Submitted (06-APR-2002) Genome Analysis, Institute of Molecular Submitted (06-APR-2002) Genome Analysis, Institute of Molecular Submitted (06-APR-2002) Genome Analysis, Institute of Molecular Submitted (06-APR-2002) Genome Analysis, Institute of Molecular Submitted (06-APR-2002) Genome Analysis, Institute of Molecular Submitted (06-APR-2002) Genome Analysis, Institute of Molecular Submitted (06-APR-2002) Genome Analysis, Institute of Molecular Submitted (06-APR-2002) Genome Analysis, Institute of Molecular Submitted (06-APR-2002) Genome Analysis, Institute of Molecular Submitted (06-APR-2002) Genome Analysis, Institute of Molecular Submitted (06-APR-2002) Genome Analysis, Institute of Molecular Submitted (06-APR-2002) Genome Analysis, Institute of Molecular Submitted (06-APR-2002) Genome Analysis, Institute of Molecular Submitted (06-APR-2002) Genome Analysis, Institute of Molecular Submitted (06-APR-2002) Genome Analysis (06-APR-2002) Ge
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                                                                                                                                                                 Submitted (24-MAY-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany
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AC117079.1 GI:20066269
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YSHSLLEDKFNRMKSSLWSICGKLAHEHKLPFKIKMKKWWKCCGHVTDELLIKEHDDY
NSIYNYINNESSSREQELIFLNMKHSWTTFTMETFIKCKISLENNMRNVTN"
a 1191 c 943 g 4950 t
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in ordered pieces.
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NOTE: This is a 'working draft' sequence.
This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                   the finished sequence as soon as it is available accession number will be preserved.
                                                                                                                                                                                                                                                                                                          FRFWTHTKSIPFLNADSLYFIVMKFDNIDRIEEIIQFLLLERCEVTVLKLLEVAIESG
RIETVNYLLSNYLQELTNQGPLKTYYTIFQFNNLSILNIFLSNEIYKSLLALYEINSE
IQYSDSESFKFINGTYEKDFYNKSFKYGYLSICKLLEBHYGSNNNNNQDNNSENSSSN
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                                                                    /product="hypothetical protein"
/protein_id="AAM43689.1"
/db_xref="GI:21166072"
                                                                                                                                                                          /protein_id="AAM43688.1"
/db_xref="GI:21166071"
/translation="MANNNNNNNNNNNNENKNEYLFWKVFKNKYLIKNIFYQMTIENNEFN
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/note="ORF_ID:dd_02309"
                    EKLNRNSNGGYVELTPISQSKRQRKNIGNRLVRPCDCKGTQRHVHVKCLCEWIGKCNK
                                                                                                                                                                                                                                                                               GGNNIYKLKLKTIEKAIQNDHIEIIKYYYLNYPQYKYLIKYSLRKLKPLDFNYFKW
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                                                                                                                                                                                                                                                                                                                                                                                                 IYNCKDCFEIFTKLSDSFIETIRATLYFENPAEQKQSDYETLNENCIFLMDLNLLDYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDLVPSKIKIIDKNNNNNSNNNNKKIKNKINNGYINIDSDIDNDNNNNNNNNNNNNNNNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YLKIDRKKCNVNSRIKINRITHLEWLTRNGYNGYYKGDDLLNDKIKSKRRLRVDRDAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="hypothetical
                                         'translation-"MLIECRFCLEEIEVEDPIYDKKEFNLNENSIKSKDIEIEELEFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIFLEKSKGDRRTISKLFNYEINKEDFKMLDLIKQSIRANNFTAVKFFSGGDNEENDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="ORF_ID:dd_02313"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db_xref="taxon:44689"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain-"AX4"
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KFGGTFLAYKGEPFLYPATFIVVIKRSNQTFQSLDIITTARLAVHVNKTTLIASLDEE
TNKPIYIAINWKGVS®
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COMPLEMENT (join(15910, 15915,16125...16229,16310...16392,
16502...16576,16692...16710))

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HSKWTVSNLHPKSYIPLOPKN"
complement(join(14375 . .14423,14526 . .14851))
/note="ORF_ID:dd_02323"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="ORF_ID:dd_02317"
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KLFESDFDQYFNSDSASIFSSCKLKNQDEKFSSFVCHSSLYSPNVLNSNNNPNNQQQV
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MLMLPSTLPQONSKIYYGYDTILNNHINNNNNNGVGSGSGGSGTGGATVNSLLFNNF
NGGIISFSNEYSGGGMFMNYNPLVGINGDTTTAGYNPGFLNSPSYSYYSFYPSSSSPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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CDS

CDS

Matches Query Match Best Local CDS

CDS

CDS

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Local Sinhes 415;
                                              Similarity
             Conservative
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LEGSLGVKGENYLMDALQINSDHRALMVVVIFLFWLFYIGLNLFAVEYFDWTSGGYTH
KVYKRGKAPKLNDVEEERNQNQIVKKATDNMKOTLKNHGGLESWKSISYTVPVAGTNK
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LIGTLETGVGISVEEEKRLTIGVELVAKPQLIFLDEDTSGLDAQSSYNIIKFIRKLAD
                                                                                                                           AGMPLVCTIHOPSSVLFEHFDRILLLARGĞKTVYFGDIĞDKSKTLTSYBERHGVRPCT
ESENPAEYILEATGAGIHGKTDVNWPEAWKQSSEYQNVVNELDLLRTKEELGKYILDS
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YDLKNSSSDQQQRIFMSWEAMILGVLLIYLVLPMFFIQKEYFKRDTASKYYSWHAFSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MKHAQLEYEKQVEQQKPSVDFKEQVLNEKSRTTSKNSEYSSSFYAQTIALTQRQLSLT
WGDKFTLTSRFLTILVLSFIFGGIYFQQPLTTDGLFTRGGAIFTSIIFNCILTQGELH
GALSGRRILQKHKSYALYRPSAYFVSQILIDIPFILVQVFLHSFIVYFMYGFEYRADK
                                                                                                                                                                                                                                                                                                                                                                                                                                           PFIFCFTLVGVSLSSASLFRGFANFTPSLFTAQNLMNFVFIFEVNYFGYSQTPDKMHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AASAYDYAKSLRIMSDTLDKTTIASFYQASDSIYNLFDKVIVLDKGRCIYFGPIGLAK
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DYDSINNIEEKFENVSKELEGQSIKFREIDGGKNNNNHDIELGERKPENEEDFKLRQY
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                                        43.8%;
             0
                                 Score 60.8; DB 2; Pred. No. 0.17;
      Mismatches
   522;
                                                                  Length 129360;
Gaps
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JOURNAL
REFERENCE
AUTHORS
TITLE
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TSP418778/c
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTATTAAAAGGAGCATAACGAGGCAACAAAAGTAATGAACACGGAGAAACAAAAGCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAAAAAAACAATAAAAAAAAAAAAAAAAATAATAATACTTGAAATGGGAATAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (05-NOV-2001) Adam G., Pflanzenschutz, Institut fuer ANgewandte Botanik, Ohnhorststrasse 18, 22609 Hamburg, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heinze, C., Willingmann, P. and Adam, G. Short intergenic regions of the S RNAs of Tomato tospovirus -not a species characteristic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N gene; N protein; NSs gene; NSs
Tomato spotted wilt virus.
Tomato spotted wilt virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 3364)
                                                                                                                                                            /PIOGUCT="NS PIOTEIN"
/PIOGUCT="NS PIOTEIN"
/PIOGUCT="NS PIOTEIN"
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/PIOTEIN 1:0429082"
/PIOTEIN 1:0429082"
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ATVNTNGVKHQOHLKVLSPDQLHSIGSTMNNSDIKDREQLQEEDI IPMDRYIEDAKG
SLSCVKEHTYKIETCYNGALGKYNLYSPNRVHEMLYSFENSENOVESUNGTWNTWNSLAK
SLSCVKEHTYKIETCYNGALGKYNLYSPNRVHEMLYSFENSENOVESUNGTWNTWNSLAK
RSLLTSAENNIMPNSQAFVKASTDSHFKLSLWLRVPKVLRQVSIQKLFKVAGDETNKT
FYLSIVCIPNHMSVETALNISYICKHQLPIRGCKAPSELSWYFSDLKEPYNTVHDPSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ssRNA negative-strand viruses; Bunyaviridae;
                                                                                                                        KYFLSKTLECLPSNTQTMSYLDSIQIPSWKIDFARGGIKISPQPVSVAKSLLKLDLSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /virion
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism~"Tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                             function="structural protein"
                                                                                                                                                                                                                                                                                                                                                                                                                             'isolate="10HK96"
                                                                                                                                                                                                                                                                                                                                                                                 country-"Bulgaria"
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                                                                                                       ement(2436.
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us NSs gene and N gene,
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Quality: Phrap Quality >-40 99.7% of Sequence:
Estimated Total Number of Errors is 2.7.
                                                                                                                                                                                               Direct Submission
Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Jun 1, 2001 this sequence version replaced gi:12830142.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                   Submitted (12-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 171317)
                                                                                                                                                                            www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                     DOE Joint Genome Institute and Stanford Human Genome Center
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DOE Joint Genome Institute.
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1 (bases 1 to 171317)
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IKKMSVISCLfffknrgsimkvikqsdfffgkitikkfsdrigatdathtffkldsmirv
RLVEETGNSENLNTIKSKIASHPLIQAYGLPLDDAKSVFLAIMLGGSLPLIASVDSFE
MISVVLAIYQDANTKDLGIDFKKYDTKEALGKVCTVLKSKAFEMNEDQVKKGKEYAAI
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∕organism-"Homo sapiens'
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RS Muzny, D. M., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, Z., Chowdhry, I., Christopoulos, C., Cheveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Ehlaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratte, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Haylak, P., Hawes, A., Hernandez, J., Hennandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Hachs, J., Jacobson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L., Li, J., Liu, W., Loulseged, H., Lozado, R.J., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* consists of 60 contigs. The true order of the pieces

is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
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Direct Submission
Submitted (09-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 9, 2002 this sequence version replaced gi:17941008.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 233269)
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Direct Submission
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Sequencing vector: M13;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 175720 bases at least Q40
Consensus quality: 180089 bases at least Q30
Consensus quality: 180792 bases at least Q20
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Center clone name: CH230-3H24
Center clone systematry Statistics
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Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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138; Conser
                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (16-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Aug 21, 2002 this sequence version replaced gi:22204483.
                                                                                                                                                                                                                                                                             AL732314 224635 bp DNA linear HTG 17-1 Homo sapiens chromosome X clone RP13-465B17, *** SEQUENCING PROGRESS ***, 8 unordered pieces.
                                           Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
                                                                               Center: Wellcome Trust Sanger Institute Center code: SC
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Best Local Similarity
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ACAGAAACTTCCAAATTTTTTTTTTTTTTTTTGGAACAAGAAATAACAGATAGAAAACTATTT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 223935; sum-of-contigs
Insert size: 183401; 20.9% error; agarose-fp
Quality coverage: 6.54x in Q20 bases; sum-of-contigs Quality
coverage: 8.94x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Consensus quality: 222703 bases at least Q40 Consensus quality: 223253 bases at least Q30 Consensus quality: 223562 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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                                                                                                                                     Conservative
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3853 3952: gap of 100 bp
3953 39565: contig of 32613 bp in length
36566 36665: gap of 100 bp
36666 70753: contig of 34088 bp in length
70754 70853: gap of 100 bp
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191180. .224635
/note="assembly_fragment:04008"
52985 c 53054 g 61479 t
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/db_xref="taxon:9606"
/chromosome="X"
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187709. .191079
                                                                                                                                                                                                                                                                                                                                             /note="assembly_fragment:03847
fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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/clone_lib="RPCI-13.2"
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fragment_chain:1"
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48.4%;
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141740: contig of 70887 bp in
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                                                                                                                                                     Score 59.4; DB Pred. No. 0.26;
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TITLE
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TACGCGCTCAAAGTATGTTATCTAGTAGGTGTGAATTAATAATGCATGGTGCGATTCAGAA 245
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AL034559 AL008974 AL008975 AL008981 AL008983 AL009015 AL010138
AL010143 AL010146 AL010154 AL010157 AL010160 AL010165 AL010169 AL010189 AL010207 AL010208 AL010214 AL021885 AL021888
AL139179 Z98556 Z99557 Z98558
                                                                                                                                                                                                                     On or before May 14, 2001 this sequence version replaced gi:2982540, gi:2982541, gi:2982544, gi:2982563, gi:2982564, gi:2982565, gi:2982564, gi:2982569, gi:2982569, gi:2982569, gi:2982569, gi:2982569, gi:2982569, gi:2982569, gi:29825974, gi:2982502, gi:2982536, gi:2982539, gi:2982539, gi:2982539, gi:2982539, gi:2982598, gi:2982539, gi:2982599, gi:2892599, gi:28925
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 253305)
Bowman,S., Lawson,D., Basham,D., Brown,D., Chillingworth,T.,
Churcher,C.M., Craig,A., Davies,R.M., Devlin,K., Feltwell,T.,
Gentles,S., Gwilliam,R., Hamlin,N., Harris,D., Holroyd,S.,
Gentles,S., Gwilliam,R., Jagels,K., Jassal,B., Kyes,S., McLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (17-DEC-1998) P.falciparum Genome Sequencing The Sanger Centre, Wellcome Trust Genome Campus, Hinxto
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                                                                                                                                                                      http://www.sanger.ac.uk/Projects/P_falciparum.
/organism="Plasmodium
                                                                                                                      ocation/Qualifiers
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GSYINQSLLALANCINSLASHRNISKVRVKYRDSKLTHLLKNSLEGNCLVWHANINP
SRTSFQESNNTLKYAFRARNIKLCATVQTHDNKESDIEKILKKNENLQKEYDTLLGKY
TNLKEFFFIINVINQLYKKQISCYKLENISDNMSSMELKQDITMYDQLYKMKSDEYR
KKVDSLKDLYQEEKQFLNNLFDTFLEKNLNYVINSKDVNDNNKSLLEEMIFFKHNENK
VNENFLYNEKVVDKNNYLNGNVAVDENVVDKNNVLNGNVAVDENVAVDENVM
VDENVAVDENVAVDENVAVDENVAVDENVAVDENVVDKNSDLYKEKKK
SESHKKNIKDDIEDNDKDTIKDĪHNNNSSDNNDDEYGSANSPVESTIVKEKK
KKIPINMETKKKRTMNGTKDFJHKTPYDINIYGILKKEDYSNKSNDYNTNKNIEKNNY
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GI NCTVFAYGATGSGKTYTMLDDKNQNGI VQLSLLELFT I I NEKKCRNI KVLMSFLEV
YNET I RDLLGKEKNKTLEVQED YAEVKYSNLC EL EVNNY EQAMLLI NEGYKNRKKSPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="Sptrembl:097318"
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Lerplyvdhilnyrlpkkylkdadkneykptcaegogigvynveseixlskypdkik
Lerplyvdhilnyrlpkkylkdadkneykstededogdedd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative RNA-binding protein"
/protein_id="CAB39067.1"
/db_xref="GI:4494008"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDDTIKNMNSNKISDKHNMKSNNILNNENGKINDKSKKCKNINNNNNNNNNNNNNNNNNNN
NNNNNNNSSSSSGKVDGINILNNSNTNERLHTFSGVYSLNLNDEIKIEINKKDMEKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTNNI LNYNDHTLKLI CNITENNKA ILHSNKSNLQKNNI LMPSYMQKKGTHIRETIKN
VYPNI NGEPSTSVENITNGEHFINGQYDALKNMSLNNYDHQHNNIMNNI SNKNKLFVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="kinesin-related protein"
/protein_id="CAB39023.1"
/db_xref="GI:4493964"
/db_xref="SPTREMBL:097277"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="PFC0865w, MAL3P7.2"
join(5457. .5577,5689. .5787,5923. .6077,6189. .6743)
/gene="PFC0865w, MAL3P7.2"
/note="PFC0865w, (MAL3P7.2), RNA-binding protein, len: 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="potential splice donor at 3' indicate splicing" join(5457. .5577,5689. .5787,5923. ./gene="PFC0865w, MAL3P7.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               indicate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIHLTSIDTISKIHARDLLKENKRKLENFQENIKHEHKDEVSLYVKKKKIKKKM'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKKGEYNPFHNNLTDMQNSILYNIINNNVENSPHSPRMKKNVAKMLLKGNLNTANFIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NYTNIHNNNNNMNSNPTSSVTSKKNENNNLINTLNAYSNVKVAVRIKPIGESEENIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNNNNNNQDVI ENMNEYPITSKNIYDSIYIPQINIKNIINSEEINNNNNNINDNNNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="PFC0860w, MAL3P7.1" 458. .4060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EKDKKSHKRRHKHSYDKYSSRSRSYSTSSSTDR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DDEDDDDDDSVDIKYKRHKEKRKSLTTKKYDKKEKHKRKSDHRDKHRRRENHSRHREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="PFC0860w, MAL3P7.
/note="potential splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation-"MRKTKNLNDPFFLNNYYYNKEENNPIIICSDEKERKTKIYSTNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="PFC0860w,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .4062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ovential splice donor at 3' end splicing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .6077,6189. .6743)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       end of PFCo860w may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of PFCo860w may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam:
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                MLNTKK REKSKS IT INDERKK SOKTY ENGIN INDMESKY PTHQLE DEN IN ANNAM INDER SERVER 
                                                                                      ETLETRNDTDVNKEVEININLFYNYTSIHSYAYYTNSLFNMLSDFQNILNKKSGNKNI
ILDGSTYDNIKVYEDVKGNCDMYTLLYCKENKYNYLISDIDKNI TEECNANFRLSKN
VSYNNNEEEEDDINGNINYNDSNIYLTTPKKNNKEEENHFLVKKLKKRTDTLNEPFNIK
FHEHFMRDFYINIYVFLSIVIFFCVFFERFKNEIENRKIFENFHVHQYIHYFQILLLE
YLYYFIYILCLETULYLFDYKEELFMSFCFLLLYGFIFTEFDFALSYYLFL
FFNFTFGCHISIYIFYULISYAYNBEILINLSHULVGFFRFEDSFALSHULNIKSIC
LNYKRHMKHIDEDIMYEDMSNSNNFVIFGCFKKVYNQLSGDNNLNISDGIQSVCEDSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCLKINKYYYYSWLLFYFIILFFYNIIFTLVVYFYVYKCLMNYFILFFLIYFFLMNS
LLFTIICMOFSNNSSINYIATFLLFFLFSSFRLIIHSGASNILTFFVLLIPHSSFCLS
LDFIFILIKNNIKIDYKOLFIKFENISLMHLIICSIVSFVLLICILNYIIYYKRKKMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MANTYDELYVPLSYYILQNEGGNTSKIDQANTKKPKKKEVINKS SLIIDIKPYGENTDLDEVLKLVKNITMEGLTWGKAHKKTPFAFGLFKLQVSCVIVDDL VITDELIETIENLGLDNEQLQKKKQMDDDEENYDEDDEIGGLVQSAEIISFNKL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YFFNDININLKONFINENTVDDLSFNIYFNEWYYFSFFIVLEYQFNSFILNYNADILK
KNNLLTPRYDEINELNKEREITMEYKKTDEKEYQVNNEYINENVGYDEKGGKYKTELK
LNDFFIYKMPMKSMKINAFDTFEKNIFRVVVFLCVCLFIVNICFDINKERKINIENFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MKDFLSYAENNDLNIFKLYNSEEDCLKNLKYAIELKSEDFKNVN
SLELNDDILNIHENDKNSLLYNLHTNIINLKSSEFNINDLYKDVYTENEFENIKNLKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.1e-15, 53.2% shortened exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLLSVENVNYYKKQKNVKFSYLFGLSPQSEGFKGKGLYKNAPLYNKYENKQYGNPFHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /www--potential splice donor sequence further splicing of PFC0870w" join(11431. .20416,20578. .20690)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFC0870w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8235.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGTQSYHNNNSTNSNDDQKKKNNNNNYYYYNNPDGLTTNVKYKTRVGDYALLNSNEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YYPYYTLESDKKINEKNERNEKNERNEKNERNEKNEKNGKNEKNKDILSSTNNNVVMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NPHILKVVKNTEFYKNFIKDIKNLKNENHYTQYFNDDRKKLFFYNFVKNNLVETKYSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical prot
/protein_id="CAB39024.2"
/db_xref="GI:8052275"
/db_xref="SPTREMBL:097278"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3032 aa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(11431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="putative elongation factor"
/protein_id="CAB39068.2"
/db_xref="GI:8052274"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            guanine nucleotide
VGVQRKKEQKKNRYTFFLKNFYLSNKEYKQPKENYEKNRNPFFYFIQKLFNLKRGNNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               jóin(11431. .20416,20578. .20690)
/gene="pFC0875w, MAL3P7.4"
/note="pFC0875w (MAL3P7.4), hypothetical protein,
3032 aa, revised: added 3' exon, possibly spliced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene-"PFC0875w, MAL3P7.4
join(11431. .20416,20578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="PFC0870w, MAL3P7.3"
/note="revised splice donor sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="SPTREMBL:097319"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 8585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.2% identity in 141 aa overlap,
d exon 2, Pfam: match to PF00736 E
nucleotide exchange domain Score 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ι protein, PFC0875w"
2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  may indicate
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61.10"
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CDS gene

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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC114238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CEYWORDS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15652 ATATATAATAGAAAAAATAAATTATAAAATTTTAAATTATACATTATAAAATAAATTTA 156711
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Sciurognathi; Muridae; Murinae;
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Miner, E., Matchell, T., Mohabbat, K., Morgan, M., Mei, G., Metzker, M., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, N., Nguyen, N., Nickerson, E., Newtson, N., Nguyen, N., Okwnonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Pickens, R., Primus, E., Pu, L.L., Quilles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, T., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Tellalon, D., Vinson, R., Wang, O., Walliams, G., Walliamson, A., Warren, R., Washington, C., Watlington, S., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baylor Plaza, Houston, TX 77030, USA
On Jul 12, 2002 this sequence version replaced g1:20467600.
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Submitted (13-UUI-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Department Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted (07-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Sequencing vector: Plasmid,
Chemistry: Dye-terminator Big Dye: 100% of
Assembly program: Phrap; version 0.990329
Consensus quality: 128160 bases at least (
Consensus quality: 133217 bases at least (
Consensus quality: 136246 bases at least (
                                                                                                                                                                                                                                     Center project name: GQXB
Center clone name: CH230-336N7
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least Q40
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 49 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence. as soon as it is available and the be preserved. 1075 1175 2180 2280 2280 3301 3401 4593 4693 2179: contry Carlo 12279: gap of unknown 1 3300: contig of 1021 P 1074: contig of 1074 bp in length 1174: gap of unknown length 2179: contig of 1005 bp in length gap of unknown contig of 1779 gap of unknown contig of 1512 gap of unknown gap of unknown contig of 1192 gap of unknown contig of 1527 gap of unknown contig of 1120 bp in length bp in 1 ďď bp in length length length length length accession number will 'n in length length length length length

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Direct Submission
Submitted (30-MAR-1999) Multimegabase Sequencing of Washington, PO BOX 357730, Seattle, WA 98195, 3 (bases 1 to 192389)

Center, University USA

Birditt, B., Lasky, S

Young, J., Rowen, L., Madan, A., Qin, S., Abbasi, N., Dors, M., Dickhoff, R., James, R., Loretz, C., Lasky, S., Madan, A., Prescott, S., Ratcliffe, A., Shaffer, T. and Hood, L.

Unpublished

(bases 1 to 192389)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 192389)

Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Birditt,B., Bloom,S., Dors,M., Dickhoff,R., Harrison,G., James,R., Lasky,S., Madan,A., Ratcliffe,A., Shaffer,T. and Hood,L.

Sequencing of human chromosome 14

sequence AC007182

AC007182

Homo sapiens chromosome 14 clone BAC

192389 bp

DNA

NA linear PRI 25-AUG-1999 507E23 map 14q24.3, complete

HIG

GI:5708446

Homo sapiens

domo sapiens. AC007182.3

Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Bloom,S., Dors,M., Dickhoff,R., Harrison,G., James,R., Madan,A., Ratcliffe,A., Shaffer,T. and Hood,L.

Submitted (25-AUG-1999) Multimegabase Sequencing of Washington, PO BOX 357730, Seattle, WA 98195,

Center, University USA

Direct Submission

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                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. .165669
                                                                                                                                                                                                                                                                                                                                                                           /organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="CH230-336N7"
                                                                                                                                                                                                                                                                                                                                                             31280 c 30162 g 48184 t
                                                                                                                                                                                                                                                                                                                                                                                                                                             124523: gap of unknown length
132057: contig of 7534 bp in length
132157: gap of unknown length
139108: contig of 6951 bp in length
139208: gap of unknown length
149165: contig of 9957 bp in length
149265: gap of unknown length
165669: contig of 16404 bp in length.
                                                                                                                                                                                                                                                                                                      53.8%;
                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                     Score 58.6; DB Pred. No. 0.38;
                            301
                                                                                                                                                                                                                                                                                                                    BB
                                                                                                                                                                                                                                                                                         120;
                                                                                                                                                                                                                                                                                                                   2
                                                                                                                                                                                                                                                                                                                                                              7115 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                   in length
                                                                                                                                                                                                                                                                                                                   Length 165669
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                                                                                                                                                                                                                                                                                      Gaps
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                       /note="low quality data"
/note="low quality data"
complement(join(163771. .163850,163987. .164105,
167102. .167192,169586. .169663,172991. .173087))
/note="This gene, predicted by Genscan, is confirmed b
several ESTs. See, for example, W27204, AA504716. Th
nearest BLASTX similarity is to hypothetical proteins
S. pombe and S. cerevisiae."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Intron-exon boundaries were defined partly by Genscan and partly by ESTs. See T79253 and AA305338. closest BLASTX hit is to AF118637, 'C receptor.'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MPHSSDSSDSSFSRSPPPGKQDSSDDVRRVQRREKNRIAAQKSR
QRQTQKADTLHLESEDLEKQNAALRKEIKQLTEELKYFTSVLNSHEPLCSVLAASTPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="This clone overlaps BAC 2317F5, Accession AC009363
and 368K8, Accession AC009399."
      /translation-"MAQVDSGLELSWGSLFAAAAAAATAVLGARSPAMGNTLQSFRDH
TFLYEKLYTGKPNLVNGLQARTFGIWTLLSSVIRCLCAIDIHNKTLYHITLWTFLLAL
                                                                                                                                                                                                                                                                          /note="low quality data" 152740. .152850
                                                                                                                                                                                                                                                                                                                                    may be a processed pseudogene
                                                                                                                                                                                                                                                                                                                                                        complement(108122. .108422)
/gene="RPS24a-like"
/note="Similar to RPS24a. Since
                                                                                                                                                                                                                                                                                                                                                                                                                         EEESNTSKVPTAVSEDHL"
                                                                                                                                                                                                                                                                                                                                                                                                                                          TFTLNLGHLWVVFITAGTMGFFMTGYLPLGFEFAVELTTYPESEGISSGLLNISAQVFG
IIFTISQGQIIDNYGTKPGNIFLCVFLTLGAALTAFIKADLRRQKANKETLENKLQEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VFGNQLGIAIGFLVPPVLVPNIEDRDELAYHISIMFYIIGGVATLLLILVIIVFKEKP
KYPPSRAQSLSYALTSPDASYLGSIARLFKNLNFVLLVITYGLNAGAFYALSTLLNRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MVNEGPNQEESDDTPVPESALQADPSVSVHPSVSVHPSVSINPS
VSVHPSSSAHPSALAQPSGLAHPSSSGPEDLSVIKVSRRRWAVVLVFSCYSMCNSFQW
IQYGSINNIEMHFYGVSAFAIDWLSMCYMLTYIPLLLPVAWLLEKFGLRTIALTGSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="low quality data"

join(91189. 91857,134295. 134436,136828. 136968,

145845. 145912,147126. 147229,151568. 151678,

153171. 153276,153398. 153509,154059. 154114,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPEVVYSAHAFHQPHVSSPRFQP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="bzip transcription factor"
join(34899. .34961,37300. .37404,58678.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="BAC 507E23"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1999 this sequence version replaced gi:4927302.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIWHYPGEEVNAGRIGLTIVIAGMLGAVISGIWLDRSKTYKETTLVVYIMTLYGMVVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCLGAWVKLGSLKPHLFPVTVVGQLICSVAQVFILGMPSRIASVWFGANEVSTACSVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product-"unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="low quality data" 62125. .62265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="B-ATF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAD51372.1"
/db_xref="GI:5764706"
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                                           /protein_id="AAD51373.1"
/db_xref="GI:5764707"
                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_1d="AAD51374.1"
/db_xref="GI:5764708"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism≖"Homo sapiens"
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Agency: Deutsche Forschungsgemeinschaft (DFG).
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
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Db 176879 A 176879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTGTTGAAGCATTAAGAAAGCTTTGAGGAAACGTTTCTTATCACTGTTAGGTCATAGAA 176878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTAACTTTAAAATAAAAAATTTGAGTAAAATGTGTTTTCTGACTATTGAGGGGCCAAAA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGTATGTGAAATTACTTTGTAAGTGCTATACAAATGTAAGGCATTATTTTTACTGGTTT 176758
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                   Submitted (18-MAY-2002) Genome Analysis, Institute of Molecular Submitted (18-MAY-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany CDS predictions from GeneID may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis (http://genome.imb-jena.de/dictyostelium/) and the Univerity Colonge, Institute for Biochemistry I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dictyostelium discoideum.
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC117072 115489 bp DNA
Dictyostelium discoideum chromosome 2 ma
AX4, *** SEQUENCING IN PROGRESS ***, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gloeckner,G., Eichinger,L., Szafranski,K., Pachebat,J., Dear,P.,
Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K
Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG; HTGS_PHASE2
                                                                                                                                                                                                                                                  Biotechnology, Beutenberstr. 11, Jena 3 (bases 1 to 115489)
                                                                                                                                                                                                                                                                                                        Submitted (06-APR-2002)
                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                    The
                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence and Analysis of Chromosome 2 of Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Noegel, A.A
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                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                        Baumgart,C.
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//www.uni-koeln.de/dictyostelium/project.shtml
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191730. .191800
/note="low quality data"
41950 c 43606 g 5432
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173850. .173930
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163815. .164050
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52.7%;
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Pred.
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54322
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map 3426827-3542314 strain
in ordered pieces.
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGSEFIIDNCQEDGNDSYHNHHHHHHHNSKNYDQTNFLLDVKSLLLPKFNYLIKELDE
CRKSIEEIKSIKIQKKSQRYQNETTTVFRNDNSKQLIKQMYNDYHFLISKHPKAMKYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CKFKIFLKNRKONKKLKKORKKOKOEDEYEEDEEDKEEVENNYLENEKNRKNEIKLK
IKNNENYLISIIECKWKFIKETILLSIESIGYEILIRSYEILEQNSSWEVVYTELYV
ASPEVGASGEYCCMREFGTLLGVESAVVVGVLESLADSDETKGLAYIALTETLVESIL
FEVRGKPIQSEGNEFILSYATITEPEYTQDHALITTILLRAFHISLAVEVIMLSSILI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ILVLTPKSKKKKEKKLFENEKKKILIENSNLIIEGFREKFIKYNVKYSKNLNMLSTYL
KECDQEFWNKDLVSHFNQLAILLEKNHNMINSMQISIDKDISNPSCHFLLPLIPFINI
                                                                                                                                                                                                                                                        SNSSINSSKNINNNNNSTCIDSSTFTSSSSDNNSEDLIIPINRSQFIRHTSIGGTEYN
                                                                                                                                                                                                                                                                                                     FCVHQLGCLIYTFDLFINLMSNITKYIWSITKTILIERKDSNYLYNNNLNSLDNLVTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRIHFFVNLLTSFTKQQKELSTIVYTMSRCLYRQNRIYHFEMFLLILCWFLNFPKFLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IINHSSNIFTIMENQILGNYRISKTKLKIKIFLKKFKKLFNNNNNKNNKDGHDDEDDD
EIDLNKINYKKSLNYSQERILKYFKRIEKVEMEMCKEYSKIEITNDLLHLEEDSQCEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NHLWISIFLYMLFILITSGIFLSSKNDKLNWTIGKRMYFEIFSLLYVVRSPTRSPIIF
LKAGLASIITLLLVTIGCLILNPFFSSELFLRTSVKILHRSHQCNKSLLRQLELKPIN
EFKISPKRKSHKKIIKNIHSRLSNSLSNLPNLSQINNNNNNSISLSNYEIEINNNNNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="hypothetical protein"
/protein_id="AAM33148.1"
/db_xref="GI:20976559"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(6455. .9932,10028. .10041))
/note="ORF_ID:dd_03233"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YARAIFDVNYFAILNIVRSTTPYLRKOKSGLILNVSSIVGHLPKGSISSYVASKYAVT
GLTLSLEQELAPFNIKVVLLSPGGFRTIITNKEKFKLVENPIPEYYPNSTPONSLEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TQQPVSIHFPNSLKSSGNNINNTNNNYNNNNNIKNNINNNNNNSINNNYNNYNIKNN
EKSENNNEKINQMKSILNCTL"
                           /product="putative splicing factor"
/protein_id="AAM33149.1"
/db_xref="GI:20976560"
                                                                                                                                                    join(10546. .10804,10924.
/note="ORF_ID:dd_02343"
                                                                                                                                                                                                                                NMSTLNRVSNCLNIPMN"
                                                                                                                                                                                                                                                                                                                                                                                               PKEIFQETMRPIFLEIRSLITNQRSLMFNSRFELLFNKQKYKDLKSLLNNISSEYMVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mknfkylfkviskrQsgeTykTiTfyscfisfTiClslfleifk
fsreffeffyIIIyvTlfTSTIVSSSDsfnvIlkTafEmmIscIVgDIVAyTIFSIff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WKELALSTDRS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAM33147.1"
/db_xref="GI:20976558"
/translation="MDPINNIDRVFLVSGTSTGLGLSIVKRLLDNNYKVAAFTRSKLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="3-OXOACYL-(ACYL-CARRIER PROTEIN) REDUCTASE
1.1.1.100). 6/101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="hypothetical protein"
/protein_id="AAM33146.1"
/db_xref="GI:20976557"
translation="MENKRKQKDEIVLVNGSNDTTPNKKQKNELQVVSSGGGREIILG/
                                                                                                                                                                                                                                                                                                                                                                                                                                     LPYYDHRELEINLLDISIKQLEAFKSIFNHNSHWFDINNNRNIDDLTSISTVSSMIMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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/note="ORF_ID:dd_02345"
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/strain-"AX4"
                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |GLMNTSNGDPNKFANAILKLDLIHQQGNKLPSNIFFGSDALEGSSHFFKSLIDESNQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'db_xref="taxon:44689"
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                                                                                      /translation-"MSAQRQFSEDLMDKFESVVKKVDNGKIFTQQLSKFLSKQQQIES
AYAKSLVKLCKDKSFAPEVEMGTLRDSFQCYREQLELIGALHEFSNRLEKLVTIGIB
GYLEESRKQRKALIANGEKCTKDLKTADESNGSKAKQNYEKLKKKQEBANEDLSKQPPG
AKEQKARKTLESATKAADKGDNEYRESVKCLQQNQQKFYHEEMFRILDDLQRFEYERI
DKSKOMLMEVITQNELYPPAVIIHNENIKKGIESIDRERDLQNYILVTMSGAQKPPEA
QYEPYQSGGFAIVNSSSNSULNISRSGELNGGGSIQNGASIISSPQQPQYQNIDHQ
TPPQPNIIQOGQQSNNNNNTNNNSWTTPPPPQPDQQQQLPQPTQLNNPPQPPIS
TYPQNIIQOGQQSNNNNNTNNNSWTTPPPPQPDQQQQLPQPTQLNNPPQPPIS
TSKNDSSNSINSINSINGEIVRALYDYNATEENEISFKANALIKVYLRDESGWWQGMVIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSRISDAKLTSHWHEALLTSIFAVSAPIGIAIGVGVASSLNVNGPTYLIVQGVFDSVC
AGILLYIGFSLMIKDFPEDMEELCRGKKYEYFLRAGLFIGLWVGAAMMAFIGKYL
join(19682. .19960,20123. .20209,20353. .20607,20740. .208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAM33191.1"
/db_xref="GI:20976602"
/dr.Thkeakkhlsssndnislhdvhtpgggddhtpggdehskshchapsgahgshvhgglindpaalktieayileegiivhsveiglavgvvddstlkallvalafhqpfegvalglindpaalktieayileegiivhsveiglavgvvddstlkallvalafhqpfegval
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VKTIRKETGGTVKLQLMDTAGQEFKSJTQTFYRGSHGVIVVZDVTDFKSFERCKNW
VEDINOYTQDKIILLVGNKSDMVADAKVTFEGQGEMAEQLKTKFLEVSAKENNGVTQ
VFDLLVQDIEATMKNSKVAQNQLNLNSEVGQKRGCC"
Join(15211. . 15350,15458. . 16451)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(22366. .2396
/note="ORF_ID:dd_01650"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MNNNPIIKNYKKSLSQSFDDLLVNKDIDDSFTCPICLKLLIDAR
QGCSEGHVFCNNCITSWLKNKNNCAVCRLHISQNCLSKNRFLESNIKKIKVFCPNKND
LNDLNDDSDGCPEILEIGNVESHSLKCIHRFVLCQYGGDKCGPVRLNKLLSHEIECPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(21183. .21470,21613. .21894))
/note="ORF_ID.dd_01649"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDDKDQLFVIIDFSEDILKLVYEEPKVEKEKEKEKEKEESQSFIGKYWFYLLPLFLII
LVNWAAPPPAAQTNAAASQGAGSRNNNNNN"
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/note="ORF_ID:dd_01647"
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GHKGTILELHWSTDSNEIYTAGYDKSIGVMDSNKGELIKRIREIKOVNNSCCEPARRGP
PLVASGSDDRSARIFDTRSKGSTHLFOHKYPYTSVCTSDASQOLITGGIDNVIRVMDI
RNQEDPLYTLAGHQDTITSTSVSKDGAYLLSNSMDNSCKIMDIRPYAPPNRNIKTFNG
                               DEGWFFGSNESNVSARFPSNYVQVI "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="mkfnkitiisivialftiilQisesitvsnlnnqkdieftmyhn
EDQSKSCKILFKPKLIPHSTNSITSVDSINFKKAIQIKCKNSLTKESRSLYQKSCDLF
KTTVVSDKDPSNLSFSSLPKGNLNDSSLQYEFLKINLDSNNMNIVASNYQLKKSPPVT
                                                              ESDRIGVFPSNFISDSSDSSKKRVDVAGRKCKVLYDYRTDCEGELNIKEGEILTIEYE
                                                                                                                                                                                                                                                                                                                                                         /product="Sequence 3 from Patent W00075321. 6/101"
/protein_id="AAM33153.1"
/db_xref="GI:20976564"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="hypothetical protein"
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/db_xref="GI:20976562"
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/protein_id="AAM33150.1"
/db_xref="GI:20976561"
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 13589)
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26525,26681.
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REMARK
REFERENCE
AUTHORS
TITLE
                                                                                                                                               COMMENT
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SOURCE
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AC115575/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTTAACAGAAACTTCCAAATTTTTTTTTTTTATGGAACAAGAAATAACAGATAGAAAAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTTAAAAAATTATATAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (21 MAR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany CDS predictions from GeneID may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis (http://genome.imb-jena.de/dictyostellum/)
                                                                                                                                                                                                                                                                                                                                                         Gloeckner, G., Eichinger, L., Szafranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J.F., Guigo, R., Kumpf, R. Tunggal, B., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A. and
                              (http://www.uni-koeln.de/dictyostelium/project.shtml
                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                       The
                                                                                                                                                                                                                                                                                                                      Sequence and Analysis of Chromosome 2 of Dictyostelium
                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1. (bases 1 to 27291)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dictyostelium discoideum.
Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC115575 27291 bp I
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                                                             the Univerity Colonge,
                                                                                                                                                                                                                                                   Dictyostelium Genome Sequencing Consortium (bases 1 to 27291)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTGS_PHASE2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCING IN PROGRESS ***, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LFMHNMLIRPANREELRNFGEBDYTIYNAGQFPANRYTKGMSSSSIAIDFARKEMYI
LGTQYAGEMKKGILTIMMYLMFKMGVLPLHSSCNQARNNGDTTLFFGLSGTGKTTLSA
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ANQVMYHFIQGYTAKYAGTEVGVTEPTATFSSCYGEBFIVWHCTKYAEMLASQLHKHS
ARAWLINTGWTGGSHCYGSRIKLAYTRAIIDAIHSGELEKIPTTKMDVFGFQVPNSCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVPSEILMGINGWADKEKYVSTMHKLAKLFIENFKKFQDKASPELVAAGPILPQ"
join(28969. .9084,29176. .99317,29453. .30610)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="mmqavaesinksiksstadytpkgyhitelesdsiyldehpsgn
akifhhdavavlyedalafehgsaitstgalytrsgyktgrspkdkrivkepssgddi
wwgpyniamddlsfminreraldylmiqekiyyidgyagwdpxyrikvryicarayha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="ORF_ID:dd_00794"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="Sequence 3 from Patent W00075321. 6/101"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="ORF_ID:dd_01651"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 58;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                   Institute for Biochemistry I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
0.52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NA linear HTG 21-MAR-20
2 map 1180800-1208089 strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ordered pieces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
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* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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/protein_id="AA192191.1"
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SQPYEKNVGFIDSVWLSSKNIRSDDFGLIGQGTIKNOVISINSFIYLPDPPIKCPEI
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/codon 
                                                                                                                                                                                                                                                                                            LKCPGGSIMTYSRNENRCLASPTCTQSSFCTLGMPLCPAGYRLDQFRATEANGCPKYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NNGGKLEFNCDANFLIDTY"
join(6320. .6707,6802. .7274)
/note="fore_ID;dd_00017"
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ETWSEVDTFLEERJENGTFPGCVALVGNOKGVLYASAKGSFTYGIGTDINDEKVPPME
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QQQLLLNKISINKLIVNEKSPLSKIKHFFINESNNIIVYGSIYKNINCNDLNYIRYY
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                                                                                                                                                                                                                                                        oin(7879. .8275,8373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPKSIKCNSQSIITNSRDFNRCLTNSTCTPLAFNGNTTVVIPIYPTCPKGYYLTFFTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MTDNNIFGNTKRFNDSIELINKLETPRFQKILTRVNERIFTESE
ENILONLFKITSLEFKGILECCSFIFEQTAYYSLSPNNLVNQLKKTMLNDDKTSCFQS
VWEDNSEHVLNFLRTQSIAPLQLNEIGWRLHYQMSSSTAIKRNASAIWELNFNNNNNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(2838. .3347,3546. /note="ORF_ID:dd_00013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(3837. .3886,4358. .5195)
/note="ORF_ID:dd_00015"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="HSPC305 (FRAGMENT). 10/100"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KTWMHLGYTGTMLCGDPERELIVILLTNRVYPDPSNIKIENVRKPFSTLVQQVYDSII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(163. .380,1237. .2062,2157. .2468))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /map="1180800-1208089"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="AX4
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KGTTYAPHY ITEAELLTAMDINIK IGTDATMATHIQTIQDRFYYKKIGENQFYPSNLGV
SLVASYELMGFEFSKRULRAA IEADUDKI SRGOKTKOEVLLSTIEKYKQLYQLANDI
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HKKPPHCFQCTPENCNLATGNKQOQOQQQQQQOTNYNRNNINNNTNSARPITTRTTRT
TTQHRTFTASINNNFNNNNFNSDRNNNNPIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILNNSNNNSSGKEIISYGPCQFPTLGFVVERYFRIVNFKPEDFWHLSVVHEKMDTSSG
KMIPVTFSWCRNRLFIDYTAAFILYEKCLDNTEATVDDYTSKESXRPVPLTTIELQKA
ASKKLRISSYQTMQYAEELYTKGLISYETETDSFQAGTDLKGLIGNQASNEFWGAXS
SRLINNNQFVYPKSGKNNDNSHPPIHPTSSATGLSGNLKKIYDFITRRFLACCSEESV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(13472. 15871,15996. 16082))
/note="ORF_ID:dd_00009"
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                                                                                                                                                                                                                                                            SVKEQKYYNVEELSMECSSDCLVKSKLYASTLDETAVYLRNVESKKILPTEQTLISSQ
TKTQSQTQTQSQQAPKPASKPIEFLNKFEKSLVITENENASLIPPNLTFDKNVDNEKT
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QLSNLKLDSSNNSTTINNTTNTTINTLNKPNVQkkSDILKKSIKEKIHFDKLTYDAQM
SLIEDETTENELRSHYYNLFQPDHFKDVVAERSASGKCGYPCCSKPLGVKKLNQKYFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(16447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NILNENDCEMTETSVTGHLMEIDVVEQEKPWASCDPIQLEDAPIRKTVPSDKEPLKKT
LEREIKKADILILWLDCDREGENIAFEVLEVCKNAKKKFEFYRAHFSAIIPREIDRAC
KNLAKPNEKDSIAVDTRMEIDLRIGAAFTRFQTLYLKKFKIISNSDNQPKTTTPANGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MLKNTFITLIFTIISISICFGSQLPTNYYFKVTHVPIYCITTPC
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VKRVKKQLFQGNALTSUKYYMFASSGIVCITTPCPSVSAILLUIDNAATNVNDVKQP
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LKCQGGHYTVYFERDSNRCLTNPQCSNDNDTRACILSIPTCSTGYDLVSYTSISTCPAY
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JOIN(1238. .18622,12711. .13189)

/note-"ORF_ID:dd_00008"
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SCLKLLQDNNIKTIFNLDNNQLFNIQQVTNSSVILNSITSNITKNSSSSGGSIFGNCN
LNILFEKQSEYYIEIKNNNCKICTFLLKAPSIFIIEEVQRSLNDSISILSLIVKSKKF
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etikileqiistslsskilnsyvkqftrycfeaisiikeiykhuddhddddddngfdg
                                                                                                                  DKFENLVKECNFDMETLKVFQDLLIQGYQ"
                                                                                                                                                                                                   {	t EDDTLLGDEQDDAPMVLNEDEDENDNNINEDEEDENKSDKSEDEFSLFRPTQMSSKRV}
                                                                                                                                                                                                                                    KIDKQPQKSTTTNKTISKPKKKTIITDDLKVPIEKKEIKIRDSDDEEDDDDSDLNYYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAL92194.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(8905..9372,9507..9941,10051..10237,
10316..10739,10891..11140))
/note="Oke:Tb:dd_00019"
/codon_start=1
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/protein_id="AAL92193.1"
/db_xref="GI:19569874"
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                                                   /note="ORF_ID:dd_00012"
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/db_xref="GI:19569873"
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                                                                                                                                       Plasmodium falciparum.
Plasmodium falciparum
Eukaryota; Alveolata;
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Plasmodium falciparum chromosome 12
Unpublished
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KRVNDLLLEIKYSSPEQKRQLAQSKLEQDVLKDDHLTYFDQPPPPQIKTIYYPYPQP
IPQPRYVNNEPTIPSESSPEDDYNSSMENNGKRPTTTTTTSNQPFQNLDFRNTA
ITPESSNPFFYDQNYSQGLMKTRPEEESARKLKELFPNTSDEVYRYVLLSTDNMMSLA
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complement(join(22953_.24207,24333..24994))
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/note="ORF_ID:dd_00014"
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Pred. No. 0.
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Indels

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69

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1 (bases 1 to 169546)
Hyman, R.W., Fung, E.L., Qin, F., Rowley, D.,
Kurdi, O.B., Conway, A.B. and Davis, R.W.
Plasmodium falciparum 3D7 chromosome 12
                                                                                               Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                      clone 3D7,
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3D7, ***
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SEQUENCING IN
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BASE COUNT
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                                                                                                                 312 GTTTTCTGACTATTGAGGGGCAAAAAAAAAAAGACAATGCCAAAAGTCTA 358
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On Aug 12, 2000 this sequence version replaced gi:8810447.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Hyman, R.W., Qin, F., Fung, E.L., Conway, A.B. and Davis, R.W.
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/clone="3D7"
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/db_xref="taxon:5833"
/chromosome="12"
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23666: gap of unknown length
169546: contig of 145880 bp in length.
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Maximum Match 100%
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                                                                                                                                                           Score
                                  1101
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Gapop 10.0 , Gapext 1.0
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1101
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Match Length
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1: /SIDS2/gcgdata/
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
   6888
6107
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875
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37973
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17131
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                                                                                                                                                           В
    AAA59599
ABL70390
AAS61342
ABK31431
AAA01920
ABL32803
ABL32803
ABL34197
ABQ67094
ABL33053
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                                                                                                                                                                                                         SUMMARIES
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Human colon cancer
Human immune syste
Human immune syste
Human angiogenesis
Human immune syste
                                                                              DNA encoding a cyt
Chemically treated
Human gene regulat
Signal transductio
                                                                                                                                                         Description
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50.4	50.4	50.4	50.4	50.6	50.6	50.6	50.8	50.8	50.8	51	51	51.2	51.2	51.2	51.2	51.4	51.6	51.8	52	52	52	52	52	52.2	52.2	52.2	52.4	52.4	52.6	52.6	53	53	53	53	53.2
4.6	4.6	4.6	٠			4.6		٠					٠		4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.8	4.8	4.8	4.8	8	4.8	4.8	4.8	4.8
8085	5689	5689	5689	12405	12405	12405	6254	5880	5880	10286	10286	23695	5690	5690	3738	4041	47108	641	7459	6636	5309	5309	5309	78925	7746	7746	5940	4501	16228	16228	72049	66933	57273	54108	8170
					24	22				24	22				21	21	24	24														22	24	24	24
AAS46479	ABK28226	AAS46426	AAS45384	ABK28169	AAS61143	AAS45330	ABL33621	ABK28177	AAS46331	ABK28148	AAS45309	ABQ66981	ABK28205	AAS45368	AAA70178	AAA70170	ABK31511	ABQ56694	ABK31382	ABN80023	ABL33736	ABK40039	AAS46527	AAC89888	ABL33856	ABK40047	AAA70105	ABK33968	AAS61424	ABL70459	ABA82623	ABA82625	ABK22784	7	ABK28257
Tumour suppressor	DNA transcription	Tumour suppressor	Chemically pretrea	DNA transcription	Human gene regulat	Chemically pretrea	Human immune syste	DNA transcription	Tumour suppressor	DNA transcription	Chemically pretrea	Human angiogenesis	DNA transcription	Chemically pretrea	Plasmodium falcipa	Plasmodium falcipa	Signal transductio	Human colon cancer	\mathbf{L}	Human chemically m	Human immune syste	Human chemically p	Tumour suppressor		Human immune syste	Human chemically p	Plasmodium falcipa	Human DNA for stag		cally trea	HBM gene	HBM q	high	Human high bone ma	DNA transcription

ALIGNMENTS

DWF4; cytochrome P450 enzyme; brassinosteroid; 22alpha-hydroxylation; plant phenotype; cell elongation; ss. AAA59599; exon exon TATA_signal promoter Arabidopsis sp. DNA encoding a cytochrome P450 enzyme designated DWF4. 14-NOV-2000 (first entry) AAA59599 standard; DNA; 6888 BP. intron intron /*tag= a
3060..315
3060..315
/*tag= b
3203..6110
/*tag= c
/product= "DWF4"
/note= "contains introns"
3203..3423
/*tag= d
3424..3503
/*tag= e
3504..3828 350* /*tag* 1 3829..3913 Location/Qualifiers

a

exon

3914..4066 /*tag- h 4067..4164

exon intron

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11-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200047715-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3'UTR
                                                                                                                                                                            The present sequence encodes a DWF4 polypeptide. The polypeptide is a cytochrome P450 enzyme that mediates multiple steps in synthesis of cytochrome P450 enzyme that mediates multiple steps in synthesis of prassinosteroids. Specifically, it mediates multiple brassinosteroids. The DWF4 22alpha-hydroxylation steps in brassinosteroid biosynthesis. The DWF4 polynucleotide is used for altering the phenotype of a plant. DWF4 polynucleotide is used for altering the phenotype of a regamble plants display a dramatic reduction in the length of different organs, and this size reduction is attributable to a defect in cell elongation. The DWF4 polynucleotides and polypeptides can be used in diagnostic assays and to generate antibodies, which can be used to produce
                                                                                                                                                                                                                                                                                             New isolated \text{dwf4} polynucleotide useful for altering the phenotype of plants, for diagnostic assays and in the production of antibodies -
                                                                                                                                                                                                                                                                                                                                                         Azpiroz R, Choe S,
                                                                                                                                                                                                                                                                                                                                                                         (ARIZ-) ARIZONA BOARD OF REGENTS
                                                                                                                                                                                                                                                                                                                            P-PSDB; AAB07921
                                                                                                                                                                                                                                                                             Claim 3; Fig 10A-G;
                                                                      2102
                                                                                                                                                Sequence 6888 BP; 2294 A; 1010 C; 1193 G;
                               2162
                                                                                                                                                                  assays and to generate antibodies,
61
                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                        2000-549142/50.
                              100.0%;
milarity 100.0%;
Conservative 0;
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99US-0119658.
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5111..5864
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6011..
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                                                                                                              Score 1101; DB 21;
pred. No. 1.6e-208;
); Mismatches 0;
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                                                                                                                                                         0 other;
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                                                                                                                                     Length 6888;
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RESULT 2
ABL70390/
ID ABL7
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AC ABL7
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ABL70390 standard; DNA; 6107

ВP

ABL70390;

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                                                                                                                                                                                                                       ATCCTAAGGGTAATTTTGGAAATCCCAATTTAAACCGATTGAGACCGTACCGGACTTCCT
                                                                                                                                                                                                     AGGGGTCCTTCTGACATTTTCACTGTTCTACCCCTACTCGTGAGCCCCACCCTTTTCCCCAT
                                                                                                                                                                                                          AGGGGTCCTTCTGACATTTTCACTGTTCTACCCCTACTCGTGAGCCCACCCTTTTCCCAT
                                                                                                                             ACTCACAACTTGATCAGATAAAATTTCATAAACACTTTTACGATGGATTCGTACGATCTA
                                                      AGTATTAAAAGGAGCATAACGAGGCAACAAAAGTAATGAACACGGAGAAAACCAAAAGCCAT
                                                                                               AGAGAGAGAAACTAGCTCC
                          CAGTAGAAGTCCGATTCCCAATCTTAAAGACAAAGCCATTAGAAAGAGAAAGTCAGTGAG 1080
                  AGAGAGAGAAACTAGCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                      CC The invention relates to a nucleic acid comprising a sequence of at least CC 18 bases of a segment of chemically pretreated DNA of genes associated CC with cell signalling. The activity of the modified sequences of the CC invention may be described as cytostatic. The object of the invention is CC constanting, as well as oligonuclectides and/or PNA-oligomers for CC signalling, as well as oligonuclectides and/or therapy of genetic and CC epigenetic parameters of genes associated with cell signalling. The CC epigenetic parameters of genes associated with cell signalling. The CC chemically modified DNA provided by the invention is useful for diagnosis and/or therapy of diseases such as sociat tumours and cancer. The sequences CC given in records AHI/7011-AHI/7012 represent chemically pre-treated CC Note: The sequence data for this patent is not represented in the printed CC specification, but is based on sequence information supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                              Matches 164;
                                                                                                                                         4651
                                                                                                                                                                                                      4711
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6107 BP; 1604 A; 136 C; 1251 G; 3116 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signalling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 280; 24pp+sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-154758/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                      86
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cancer; tumour;
                                                                                                                                                                                                                                                                         (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chemically treated cell signalling DNA sequence complementary to#140.
                                                                                                                                                                                                                                                                                                                                               Local
TAAAACTCATAATTTAAAAAAAAATAACGAAAACTACTTATTATTATCACTTTTCTTTTTCC
                            GAATTAAAATATTAAACTTTAAAATAAATAAAATTTGAGTAAATGTGTTTTCTGACTATT
                                                                                                                                                                                      TTAAATAAAAAACTAAAAAAAAACCACTAAAAATTTATAATTACAAAAATCAAAAATTTT
                                                           TAAAATAAAAAAAATAATTAATTCATATATCATAACAAAATTACTAATACTATCTAAAAT 4532
                                                                                   TCTAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAATTGGGACAACAATGAAAAACG
                                                                                                                        AAACTTAACTATATAAAACTCATATAACTAAAAAAAACGTAAAAAAATAAACTAAAATAAAA
                                                                                                                                                      AATATACATTAAGCAAATTTTAAAAAATTATATAAGCCTATACGCGCTCAAAGTATGTTA
                                                                                                                                                                                                                     TTTTTTATGGAACAAGAAATAACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGT 145
                                                                                                                                                                                                                                                   CAAAAAAATAAAATAAAATAATAATAATAAAAAAATCTAAAAATACATAAAATATCCTT 4712
                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                            Conservative
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2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytosine methylation; cell signalling disease;
                                                                                                                                                                                                                                                                                                                                        5.1%;
47.8%;
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                                                                                                                                                                                                                                                                                                                     0; Mismatches 179; Indels
                                                                                                                                                                                                                                                                                                                                      Score 56.6; DB
Pred. No. 0.044;
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                                                                                                                                                                                                                                                                                                                                                      DB 24;
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                                                                                           265
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The invention relates to 224 nucleic acid sequences comprising at least 22 18 bases of a chemically pretreated gene associated with gene regulation 22 selected from 43 known genes (or complementary sequences). The 23 chemical pretreatment converts cytosine bases unmethylated at the 24 dissimilar to cytosine, to enable analysis of cytosine methylations. 25 chemical pretreatment converts cytosine bases unmethylated at the 26 dissimilar to cytosine, to enable analysis of cytosine methylations. 26 cm 27 cm bn Ma sequences, oligomers (or sets/arrays) and method are 27 cm bn Ma sequences, oligomers (or sets/arrays) and method are 28 cm secolated with gene regulation and in therapy of such diseases, by 28 cm abling analysis of the cytosine methylation patterns of such genes, 29 cm abling analysis of the cytosine methylation patterns of such genes, 29 cm and therapy of e.g. severe combined immunodeficiency disease, cardiac 29 cm and therapy of e.g. severe combined immunodeficiency disease, cardiac 29 cm and 20 cm and 20 cm asyndrome, 30 cm and 20 cm asyndrome, 30 cm and 20 cm asyndrome, 30 cm and 
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AAS61342/c
ID AAS61342 standard; DNA; 6107
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                              ftp.wipo.int/pub/published_pct_sequences
                                                        of the printed specification, but format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-APR-2000;
07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-017470/02.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; Gene regulation-associated gene; severe combined immunodeficiency; cardiac damage; inflammatory response; Haemophilia; Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; Preclampsia; cardiac allograft vascular disease; colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour; immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-APR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene regulation-associated gene oligonucleotide #297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; 2000DE-1019058.
; 2000DE-1019173.
; 2000DE-1032529.
; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ID No 304; 26pp; English.
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Sequence 6107 BP; 1604 A; 136 C;

1251 G;

3116 T;

0 other;

Similarity

5.1%; 47.8%;

.044; DB 24;

Length 6107;

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ABK31431/c
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signal transduction associated genes. The DNA sequences are chemical modified using a solution of bisulphite, hydrogen sulphite or disulphite. Also disclosed are oligonuclades and/or PNA oligomers for detecting the cytosine methylation state (CpG islands) of these genes, and a method for the diagnosis and/or therapy of genetic and
                                                                                                                           Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction \,
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                                                                       The present invention relates to chemically modified DNA sequences
                                                                                                    Claim
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                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                in; signal transduction associated gene; cytosine methylation
island; signal transduction associated disease; solid tumour;
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15-MAY-1998; 15-MAY-1998; 21-OCT-1998;

98US-0085426. 98US-0085537. 98US-0085696. 98US-0105234.

99WO-US10602

14-MAY-1998; 13-MAY-1999; 18-NOV-1999

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Best Local S
Matches 164
                                                                                                                                                                                      breast cancer; oestrogen receptor-positive breast cancer; therapy; oestrogen receptor-negative breast cancer; lung cancer; ss.
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Note: The sequence data for this patent did not form part of the specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     epigenetic parameters of genes associated with signal transduction. The genomic DNA can be obtained from cells or cellular components which contain DNA, e.g. cell lines, blopsies, blood, sputum, stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as tissue from eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, and all their possible combinations. The sequences of the invention are useful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumours and cancer. ABK31158-ABK31545 represent chemically pretreated genomic DNA sequences of different genes associated with signal transduction, or the displacement genes associated with signal transduction, or
                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                  Human
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                                                                                                                                                                                                                                                                                                                                                         AAA01920 standard;
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA00010 to AAA02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.
                              ABL32803;
                                                             ABL32803
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G, Drmanac R,
itz D, Kita D,
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Randazzo F, Kennedy GC, POT D, Nassu
Crkvenjakov R, Dickson M, Drmanac S,
Garcia V, Jones LW, Stache-Crain B;
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Pred. No. 0.
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Best Local Similarity
                                     ABL34197 standard; DNA; 37973
                                                                                                         5643 CGTATCTATAAAATCTTTTTTTTTTTTTTTTTTAAAATAAAATCTCGCCCTATT 5589
                                                                                                                                                                          5703
                                                                                                                                                                                                                                    5763
                                                                                                                                                                                                                                                                                           5823
                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, ADDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psorlasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6113 BP; 1694 A; 157 C; 1445 G; 2817 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with cytosine methylation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 776; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-130909/17.
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01-SEP-2000; 2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antilnflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                        126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-JAN-2002.
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                                                                                                                                                                                                                                                              99
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                                                                                                                                   TACGCGCTCAAAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGATT 240
                                                                                                                                                                                     TGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATAAGCCTA 185
                                                                                                                                                                                                                                              ACAGAAACTTCCAAATTTTTTTTTTTTATGGAACAAGAATAACAGATAGAAAACTATTT 125
                                                                                                                                                                                                                                                                                  TCTCTTTAAAAAAATTCATAAAATAAATAAAACATAATATTTTATTTTATACGTATCTA
                                                                                                                                                                                                                         immune system associated gene SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                4.9%;
51.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                              Score 54.2;
Pred. No. 0.
                                      BP.
                                                                                                                                                                                                                                                                                                                                               Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>~</u>
                                                                                                                                                                                                                                                                                                                                                                            DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 776
                                                                                                                                                                                                                                                                                                                                                                            Length 6113;
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ABL34197;

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Best Local
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                                                                                                                                                                                        8357
                                                                                                                                                                                                                                           8417
                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                         rheumatoid arthritis, psoriasis and inflammatory/ulcerativ diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid comprising frag
for diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiinflammatory; cancer; eye disease; arteriosclerosis; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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 307
                                                                                                                                                             127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EPIG-)
                                                                                                                                                                                                                  83
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 AATGTGTTTTCTGACTA
                           TGGGACAACAATGAAAACGGAATTAAAATATTAAACTTTAAAATAAAAAAATTTTGAGTA 306
                                                                             AAATTATTAATATTTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAATTTTGTTAAC 67
                                                                                                                                  GTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGCCTAT 186
                                                                                                                                                                                                               AGAAACTTCCAAATTTTTTTTTTTTTTTGGAACAAGA-AATAACAGATAGAAAACTATTTT 126
                                                                                                      ACGCGCTCAAAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAAT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immune system associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immune
                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                   37973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 2170; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Piepenbrock C,
                                                                                                                                                                                                                                                                                              4.9%;
llarity 50.2%;
Conservative
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2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                    B₽;
                                                                                                                                                                                                                                                                                                                                                    10756 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease; cytosine methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fragment of chemically modified ment of diseases associated with
                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                    620 C;
                                                                                                                                                                                                                                                                                              Pred. No. 0.2;
); Mismatches
                                                                                                                                                                                                                                                                                                                         Score 53.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ζ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO:
                                                                                                                                                                                                                                                                                                           0.2;
                                                                                                                                                                                                                                                                                                                                                 G; 18287
                                                                                                                                                                                                                                                                                                                       DB 24;
                                                                                                                                                                                                                                                                                              157;
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                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                      Length 37973;
                                                                                                                                                                                                                                                                                                                                                   0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bowel disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene, use
abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anaemia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful
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                                                                                                                                                                    Best Local Similarity Matches 165; Conserv
                                                                                                                                                                                    Query Match
Best Local :
                                                                                                              74888
                                                                                                                                                                                                                                                                                                                        bases of chemically pretreated DNA of anglogenesis-associated genes (II) having sequences (ABQ66971-ABQ67178) or their complements. (I), also, related oligomers, are used to evaluate the methylation status and/or single-nucleotide polymorphisms, in anglogenesis-related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy, neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis, diabetic retinopathy, macular degeneration caused by neovascularisation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8117
                                                                                                                                                                                                                          Sequence 83391 BP; 24547 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid fragments from chemically treated angiogenesis-associated genes, useful for determin status, e.g. in diagnosis or treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schacht
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; anglogenesis; methylation; eye disease; glaucoma; tumour; inflammation; rheumatoid arthritis; diabetic retinopathy; antiulcerds; macular degeneration; inflammatory bowel disease; Crohn's disease; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                 Crohn's disease.
                                                                                                                                                                                                                                                                                                              psoriasis, arteriosclerosis, inflammatory bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-DEC-2000; 2000DE-1061338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-DEC-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABQ67094;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EPIG-)
                                                                                  69
                                                                                                                                         9
                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                             invention
                        TGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGCCTATAC 188
                                                                               GAAACTTCCAAATTTTTTTTTTTTTTTATGGAACAAGAATAACAGATAGAAAACTATTTTGT 128
                                                                                                           AATTATTAATATTTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAATTTTGTTAACA 68
AGTAG - AGAAATGATTACGTAAATAATAATAGTATTTTATATAATAGAATAGTATGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002-500450/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO 124; 41pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001WO-EP14320
                                                                                                                                                                                                                                                                                                                                                                                                                            relates to a nucleic acid (I) comprising a segment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                        4.9%;
49.5%;
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                                                                                                                                                                    0,:
                                                                                                                                                                                                                          665 C;
                                                                                                                                                                  Score 53.8; D
Pred. No. 0.23
0; Mismatches
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                                                                                                                                                                                                                          16953 G; 41209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of cancer -
                                                                                                                                                                                              B
                                                                                                                                                                  167;
                                                                                                                                                                                              24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ
                                                                                                                                                                                                                                                                                                              diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ID
                                                                                                                                                                                                                          T; 17 other;
                                                                                                                                                                    Indels
                                                                                                                                                                                              Length
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                                                                                                                                                                                                                                                                   part of the printed directly from WIPO
                                                                                                                                                                                                83391;
                                                                                                                                                                                                                                                                                                              ulcers
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                                                                                                                                                                  Gaps
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75066
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75187

GTAGTATAATAGTTATAAAAGAGAAATTTAAAG 75219

TGTGTTTTCTGACTATTGAGGGGCAAAAAAAAG

ABL33053;

ABL33053 standard;

DNA; 17131 BP

75127

TTATTAATATTAATGGAAAAATATAGGTTATAAAATTATATAGAATTTAATTTAATTTAT 75186

341

308 75126 248

GCGCTCAAAGTATGTTATCTAGTAGGTGTGATTAATAATGCATGGTGCGATTCAGAATTG

309

75067

189

249

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RESULT 9
ABL33053/c
AID ABL33053/c
AZX ABL3306
AZX ABL330
AZX ABL330
AZX Human;
KW Human;
KW neurop
KW antiin
KW acute
KW gene;
XX Homo s
YX Homo s
YX Homo s
PN W02002
XX Homo s
PN W0200
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                                                                                                                                       Matches
                                                                                                                                                                    Query Match
Best Local :
                                  6867
                                                                                                                                                                                                                                                                                                                    The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, macular generation, arteriosclerosis, anaemia, neovascular glaucoma and leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, humania, Altheimer's disease, AIDS, epilepsy, neurofibromatosis,
                                                                                                                                                                                                                                         Sequence 17131 BP;
                                                                                                                                                                                                                                                                            diseases. The present sequence is a gene of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 1026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUL-2001; 2001WO-EP07537
                                                   28 ATAACAATGCATAGAAAGTTCCAAAAAAATTTTGTTAACAGAAACTTCCAAATTTTTTT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; a
acute_myeloid leukaemia; Alineimer's disease; AIDS; epilep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurofibromatosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAR-2002
2002-130909/17.
                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Piepenbrock C,
                                                                                                                              Conservative
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                                                                                                                                                                                                                                5134 A;
                                                                                                                                                  4.98;
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                                                                                                                                                                                                                                                                                                   psoriasis and inflammatory/ulcerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berlin
                                                                                                                                                                                                                        253 C; 3328 G; 8413 T;
                                                                                                                           0;
                                                                                                             Score 53.4; DB 24;
Pred. No. 0.22;
0; Mismatches 141;
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                                                                                                                                                                                                                                                                            invention.
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                                                                                                                                                                                                                           3 other;
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i abnormal
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RESULT 10
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07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                         Olek
                                                                                                                                                                                                                                                                                                                                                                   PNA; cytosine methylation state; SNP; retroviral infection; gene; ds; viral infection; serie; ds; viral infection; Sezary syndrome; adenosine deaminase deficiency; cancer; inmunological disorder; syndrome; haematological disorder; tuberculosis; psoriasis; Rieger's syndrome; neurological disorder; erythropoiesis; neurodegenerative disorder; meurological disorder; erythropoiesis; myelodysplastic syndrome; myocardial infarction; hypertension; arthritis; angiogenesis; congenital heart disease; HDR syndrome; gene therapy;
                                                                                                                                                                                                                                                                                06-APR-2001; 2001WO-EP03973
                                                                                                                                                                                                            (EPIG-)
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                                                                                                                                                                                                                                                                                                                                                 Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA transcription associated gene;
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                                                                                                                                                                                                          EPIGENOMICS
                                                                                                                                                                                     Piepenbrock
                                                                                                                                                                                                                             ; 2000DE-1019058.
; 2000DE-1019173.
; 2000DE-1032529.
; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    e; peptide nucleic acid; PNA-oligomer; SNP; retroviral infaction.
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The invention relates to a nucleic acid, which comprises a segment of the chemically pretreated DNA of genes associated with DNA transcription from one of 346 sequences, and an oligomer, in particular an oligonucleotide to the chemically pretreated DNA of genes associated with DNA transcription. The set of oligomer that the pretreated with DNA cytosine methylation state and/or single nucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleic acids are useful for
                                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, solid
                                                                                                                                                                                                                                                                                                                                                                                          SEQ
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WPI;

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RESULT 11
ABK22782
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Note: The sequence data for this patent did not form part of the printed expectification but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                              lipid-associated condition; arteriosclerosis; cardiovascular disease; ss; osteoporosis; atherosclerosis; diabetic atherosclerosis; plaque build-up; neurovascular condition; wound healing; gene therapy; PCR primer; probe; bone development disorder; antiarteriosclerotic; cardiovascular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human high bone mass (HBM) polynucleotide clone #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK22782 standard; cDNA; 54108
                             26-MAY-2000;
                                                                                            25-MAY-2001;
                                                                                                                                                           06-DEC-2001
                                                                                                                                                                                                                         WO200192891-A2
                                                                                                                                                                                                                                                                                                                                                   osteopathic;
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Local Similarity 47.8%;
les 154; Conservative
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                                                                                            2001WO-US16946
                             2000US-0578900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zmax1; HBM; high bone mass gene; lipid regulation; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2772 A;
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Pred. No. 0.
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method for identifying a molecule involved in lipid regulation comprising identifying a molecule that binds to or inhibits binding of a molecule to high bone mass (HBM) or its wild type gene, Zmax1. Compounds identified by the method are useful for treating, diagnosing, preventing or screening for normal and abnormal lipid-associated conditions, including arteriosclerosis, cardiovascular disease, stroke, and osteoporosis. The compounds may also be used in the treatment or prevention of diabetic atherosclerosis, neurovascular conditions caused by plaque build-up, poor circulation due to plaque build-up and associated poor wound healing. The methods may be used in gene therapy, pharmaceutical development, and disorders. Molecules identified by comparison of Zmax1 and HBM systems can be used as surrogate markers in pharmaceutical development, in diagnosis of human or animal bone disease, and in the treatment of bone diseases. Sequences ABK22776-ABK23411 represent cDNA molecules encoding human Zmax1 and HBM, and PCR primers, probes, linkers and adapters of the invention.
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Best Local S
Matches 157
                                                                                                                                                                                                             28102
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                                                  09-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosing, treating or preventing e.g., arteriosclerosis, comprises identifying a molecule that binds to high bone mass gene or its corresponding wild type gene \,
                                                                                    ABK22784;
                                                                                                                       ABK22784 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 54108 BP; 11394 A; 14471 C; 15121 G; 13120 T; 2 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENO-) GENOME THERAPEUTICS CORP. (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
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                                                                                                                                                                                                           AAGTTGCTTTTTC
                                                                                                                                                                                                                                                                              TAATATACATTTATAAATACACATTTATATTATTTATATAAAATATATATAAAATCTCC 28101
                                                                                                                                                                                                                                                                                                               ACATACTTATAAGTATATTTAAAATATATGTAATGTATATTTTTTAATGTATGATATA
                                                                                                                                                                                                                                                                                                                                                                              TTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGCCT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACAGAAACTTCCAAATTTTTTTTTTTTTTTGGA-ACAAGAAATAACAGATAGAAAACTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 284-323; 409pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Little RD,
                                                                                                                       CDNA; 57273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recker RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 53; DB 24; I
Pred. No. 0.31;
0; Mismatches 155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24; Length 54108;
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Human high bone mass (HBM) polynucleotide clone #7

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method for identifying a molecule involved in lipid regulation comprising identifying a molecule that binds to or inhibits binding of a molecule to high bone mass (HBM) or its wild type gene, Zmax1. Compounds identified by the method are useful for treating, diagnosing, preventing or screening for normal and abnormal lipid-associated conditions, including arteriosclerosis, cardiovascular disease, stroke, and osteoporosis. The compounds may also be used in the treatment or prevention of diabetic atherosclerosis, neurovascular disease, stroke, and osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conditions caused by plaque build-up, poor circulation due to plaque build-up and associated poor wound healing. The methods may be used in gene therapy, pharmaceutical development, and diagnostic assays for boundevelopment disorders. Molecules identified by comparison of Zmax1 and HBM systems can be used as surrogate markers in pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; mouse; Zmax1; HBM; high bone mass gene; lipid regulation; stroke; lipid-associated condition; arteriosclerosis; cardiovascular disease; ss; osteoporosis; atherosclerosis; diabetic atherosclerosis; plaque build-up; neurovascular condition; wound healing; gene therapy; PCR primer; probe; bone development disorder; antiarteriosclerotic; cardiovascular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnosing, treating or preventing e.g., a identifying a molecule that binds to high corresponding wild type gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200192891-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             development, in diagnosis of human or animal bone disease, and in the treatment of bone diseases. Sequences ABK22776-ABK23411 represent cDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying molecules involved in lipid regulation, useful for diagnosing, treating or preventing e.g., arteriosclerosis, comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYCR-)
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                                                                                                                                                                                                                                                                                                                    66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                        adapters
                                                                                                                                                                                                                                                            TTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGCCT
                                                                                                                                                                                                                                                                                                              ACAGAAACTTCCAAATTTTTTTTTTTTTTTTATGGA-ACAAGAATAACAGATAGAAAACTATT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENOME THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 350-392; 409pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Little RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0578900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human Zmax1 and HBM, and PCR primers, probes, linkers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 53; DB 24;
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                        26974
                                                                                                                                                                                                                                                                 osteoporosis, Paget's disease, sclerostosis, dysplasia. ABA82038 to ABA82700 and AAG68168
                                                                                                                                                                                                                                                                                     mass (HBM) gene, which are found on chromosome 11q13.3. The Zmax1 and HBM genes have osteopathic activities. The genes can be used in gene therapy, antisense therapy and in the production of vaccines. They can be used in the diagnosis and treatment of bone disorders including
                                                                                                                                                                                                                                                                                                                            The present invention describes the human Zmax1 gene and the high bone mass (HBM) gene, which are found on chromosome 11q13.3. The Zmax1 and
                                                                                                                                                                                                                                                                                                                                                                 Claim 51; Page 308-350; 443pp; English.
                                                                                                                                                                                                                                                                                                                                                                                           New high bone mass (HBM) modulating bone mass for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-APR-2000;
05-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antisense therapy; vaccine; bone disorder; Paget's disease, sclerostosis; osteomalacia; fibrous dysplasia; ds.
                                                                                                                                                                                                                           Sequence 66933 BP; 14237 A; 17817 C; 18323 G; 16556 T; 0 other.
                                                                                                                                                                                                                                                      sequences used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carulli JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUN-2000; 2000WO-US16951.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200177327-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence tagged site;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human
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Local
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                                                TTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGCCT 184
                                                                                                                                           2001-657171/75
                                                                         ACAGAAACTTCCAAATTTTTTTTTTTTTATGGA-ACAAGAAATAACAGATAGAAAACTATT 124
                                                                                                                           HBM gene region b200e21-h_contig4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     high bone mass;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENOME THERAPEUTICS CORP
                                                                                                                                                                                         Similarity
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0543771.
2000US-0544398.
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                                                                                                                                                                                                                                                    the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA;
                                                                                                                                                                                       50.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; HBM gene; Zmaxl gene; chromoson STS; osteoporosis; osteopathic;
                                                                                                                                                                                                    4.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recker RR,
                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                            Zmax1 gene
                                                                                                                                                                                      Score 53; DB 2
Pred. No. 0.32;
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                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        genes and proteins useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Johnson
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f
                                                                                                                                                                                                    DB 22;
                                                                                                                                                                                                                                                                                                                                                                                           e.g. osteoporosis
                                                                                                                                                                            155;
                                                                                                                                                                                                                                                    present invention.
                                                                                                                                                                                                                                                                 to AAG68193 represent
                                                                                                                                                                                                                                                                              osteomalacia and fibrous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome 11; 11q13.3;
                                                                                                                                                                                                   Length
                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy;
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                                                                                                                           Best Local Similarity Matches 157; Conserv
                                                                                                                                       Query Match
Best Local
                                   30622
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                                                                                                                                                                                                     The present invention describes the human Zmax1 gene and the high bone mass (HBM) gene, which are found on chromosome 11q.13.3. The Zmax1 and HBM genes have osteopathic activities. The genes can be used in gene therapy and in the production of vaccines. They can be used in the diagnosis and treatment of bone disorders including osteoparosis, Paget's disease, solerostosis, osteomalacia and fibrous dysplasia. ABAB2038 to ABAB2700 and AAG68168 to AAG68193 represent
                                                                                                                                                                                            sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                              Claim 51; Page 258-302; 443pp;
                                                                                                                                                                                                                                                                                                                     New high bone mass (HBM) modulating bone mass for
                                                                                                                                                                                                                                                                                                                                                                           Carulli JP, Little RD,
                                                                                                                                                                                                                                                                                                                                                                                                                       05-APR-2000;
05-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; high bone mass; HBM gene; Zmax1 ge
sequence tagged site; STS; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABA82623
                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200177327-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antisense therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human HBM gene region b527d12-h_contig309G
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              125
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2001-657171/75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; DNA; 72049 BP.
                                                                                                                            Conservative
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2000US-0544398.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              osteomalacia; fibrous dysplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccine;
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                                                                                                                                    4.8%;
                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                                                                            Recker RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene; 2max1 gene; chromosome 11;
osteoporosis; osteopathic; gene 1
bone disorder; Paget's disease;
                                                                                                                           0;
                                                                                                                                    Score 53; D. Pred. No. 0.
                                                                                                                                                                                                                                                                                                                 Zmax1 genes and proteins useful for treatment of e.g. osteoporosis -
                                                                                                                                                                                                                                                                                               English.
                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                            Johnson
                                                                                                                              DB .
0.32;
                                                                                                                                               22; Length 72049;
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                                      CC The invention relates to a nucleic acid comprising a sequence of at least CC 18 bases of a segment of chemically pretreated DNA of genes associated CC with cell signalling. The activity of the modified sequences of the CC invention may be described as cytostatic. The object of the invention is CC to provide the chemically modified DNA of genes associated with cell convention as well as oligonucleotides and/or PNA-oligomers for CC detecting cytosine methylations, as well as a method which is CC particularly suitable for the diagnosis and/or therapy of genetic and CC epigenetic parameters of genes associated with cell signalling. The CC chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences CC genemic DNA's of genes associated with cell signalling.

CC Note: The sequence data for this patent is not represented in the printed CC speculication, but is based on sequence information supplied by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL70459,
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                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 349; 24pp+sequence listing; English.
                                                                                                                                                                                                                                                                                                                             Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signalling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signalling \,
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01-SEP-2000;
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                             European Patent
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APPLICANT: Etzler, Marilynn E.
APPLICANT: Murphy, Judith B.
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: A No. 6465716 Factor Binding Protein From Legume Roots
FILE REFERENCE: 023070-079810US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09129112 Patent No. 6465716
                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 3
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Best Local
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CURRENT FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: US 08/907,226
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                                                                                                                                                                                                                                                                                                                       ORGANISM: Dolichos biflorus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGAGTTATGATATAAAAAAATCAAGACATAAAATTTATAAATATTTAAATATTTAAT 2015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTAAAATTTAATAATTTAAAATGTTTTTAAAAACATAAAATAATAGTTTGGGTA-TGTAT 2195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAATGTGTTTTCTGACTATTGAGGGGCAAAAAAAAAAGCCAATGCCAAAAGTCTACGGGTTT 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TACGCGCTCAAAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAA 245
                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Ver. 2.1
                                                                                                                 exon
               (1698)..(1790)
                                                     (1617)..(1697)
                                                                                           (1560)..(1616)
                                                                                                                                                                       (1023)..(1151)
                                                                                                                                                                                                                                               (633)..(944)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            1997-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.5%;
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                    TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                               REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2637 TTTTATATTATCAATTAAGCAGACAA 2612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2936
                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251
                                                                                                                                                                                   CLASSIFICATION: 435
                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75
            STRANDEDNESS:
                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCACAACAAGTTTGAAATTTAAAACTATATTATAAATATTACCAAATACATTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCAAATTTTTTTTTTTATGGAACAAGAAATAACAGATAGAAAACTATTTTGTTGTGGA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATTTTATAGTGTTTTACTATTCAAATAAACATAATGCAGATATGAAGTTTACTG-AACT 2878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCAAAGTATGTTATCTAGTAGGTGTAATTAATA--ATGCATGCGATTCAGAATTGGG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGGAAGTAGTAATATACATTAA--GCAAATTTTAAAAAATTATATAAGCCTATACGCGC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTTTTTTTTTTTTTTTTGAAAATGTTTTGAAATATTGTCAAATATTAATAGTGA 2818
                                                                                                                                                                                                                                                                                                                                     92660
                                                                                                                                                                Israelsen, Ned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Application 5993827
                                                                                                                                                                                                                                                                                                                                                                                            620 Newport Center Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chitnis, Chetan
Miller, Louis H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sim, Kim L.
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O Newport Center Drive 16th Floor
linear
                                                                                                      (619)
           single
                                                                                    9) 235-8550
235-0176
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                                                                                                                                                                                                                                                                                                                                                                                                                                      BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                David S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08487826B
                                                                                                                                                                                                                        US/08/487,826B
                                                                                                                                             29,655
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Pred. No. 0.023;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 6265;
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RESULT 4
US-08-998-416-1137/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Meigs, J. Timothy
                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy
                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129
                                                                                NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38,241 REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                   FILING DATE: 24
CLASSIFICATION:
                                                                                                                                                                                              APPLICATION NUMBER: US/08/998,416 FILING DATE: 24-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                           APPLICATION NUMBER: CH 0016/97 FILING DATE: 31-DEC-1996
                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 AATTATTAATATTTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAATTTTGTTAACA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCGCTCAAAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAATTG 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAAATTATATAAGCCTATAC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
                                                                                                                                                                                                                                                                                                                    27709
                                                                                                                                                                                                                                                                                                                                         T: 3054 Cornwallis Road
Research Triangle Park
No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                      Wendland, Jurye...
Wendland, Jurye...
Wendland, Jurye...
Knechtle, Philipp
Knechtle, Corinne
Rebischung, Corinne
Rebischung, Corinne
NVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
NVENTION: AND USES THEREOF
TOORIENCES: 1152
                                          919-541-8689
                                                                                                                                                                                                                                                                                                                                USA
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Steiner, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Philippsen, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08998416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mohr, Christine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                       919-541-8587
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                                                                              PF/5-30306/A/CGC1976
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Pred. No. 0.12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154;
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                                             US-08-451-405A-2
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application Patent No. 5736358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                               FILING DATE: 15-JAN-19
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FL
                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: THE WEBB
                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FASEL, NI APPLICANT: REYMOND,
                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                       TYPE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    396 ATAAAAATAATAATTT 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 ATGCATGGTGCGATTCAGAATTGGGACAACAATGAAAACGGAATTAAAATATTAACTTTA 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                              APPLICATION NUMBER: US/OFFILING DATE: 26-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 TAACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTT 165
                                                                                                                                        APPLICATION NUMBER: 07/9 FILING DATE: 15-JAN-1993
                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                OPERATING SYSTEM:
SOFTWARE: WORDPEI
                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 636 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCTTATAAAAAGATTAAATAATATAAATCAACATAATATTTATAAAAATAGATATTATA
                                                                     NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                      15219-1818
                                                                                                                                                                                                                                                                                                                                                             PITTSBURGH
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                                                                                                                                                                                                                                                                                                                             PENNSYLVANIA UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08451405A
                                                                                                                                                                                                                                                                                                                                                                       E: THE WEBB LAW FIRM
700 KOPPERS BUILDING, 436 SEVENTH
                                                                                                                                                                                                                                             WORDPERFECT 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                       FASEL, NICOLAS JOSEPH
REYMOND, CHRISTOPHE DOMINIQUE
JENTION: DICTYOSTELID EXPRESSION VECTOR AND
                                                                                                                                                                                                                                                                    Midwest Micro 486-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                          UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAG1692RP
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 46.38;
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                                                                                                                                                                                                                                                                                      FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                              METHOD FOR EXPRESSING A DESIRED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301
                                                                                                                                                                                                               US/08/451,405
                                                                                                                                                        07/965,273
Score
Pred.
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AVENUE

No;

DB 1; 0.07;

Length 731;

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RESULT 6
US-08-883-795A-36
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               US-08-883-795A-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                     TELEPHONE: (416) 364-7311
                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Delcuve, Genev
                                     IMMEDIATE SOURCE:
                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                322 ATCAMAMAMAMAGGTATTTAMAGAM 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 AAAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAATTGGGACAA 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82
                                                      ORGANISM:
                                                                                                                                                                                                                                                                    FILING DATE: 27 CLASSIFICATION:
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0
FILING DATE: 27-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15
                                                                                          TOPOLOGY:
                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                           NAME: Gravelle, Micheline
                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                 ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGCCTATACGCGCTC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTATTTTATTTTTATTTTTTAAAAAAATAAAAATTAGAATAAAATATTTCTATTTGAA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCTGACTATTGAGGGGCAAAAAAAA 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACGGTATATGATAAGAAAATTCTAAAAAAAAATTCAGATAATTTTTGGATTGGAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAGTTTTTATTTGTATTTAAAATTATATTAAACATAGTGAACCTAAAAATAGATTTGTG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCAAATTTTTTTTTTTTATGGAACAAGAAATAACAGATAGAAAACTATTTTGTTGTGGA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36, Application US/08883795A
o. 5985607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151;
                                                                                                                                                                                                                                                                                                                                                                                          M5H 3Y2
                                                                                                                     nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                     Ontario
                                                                                                                                665 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                           40 King
                                                                                                                                                                         (416)
                                                                                                                                                                                                                                                                                                                                                                                                       Canada
                                                    Homo sapiens
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Vectors for
                                                                                                                                                                                                                                                                                                                        Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                             US/08/883,795A
                                                                                                                                                                                                                       40,261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Applic Patent No. 6114605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                    FILING DATE: 10-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                     APPLICATION NUMBER: PCT/
FILING DATE: 09-OCT-1997
                                                                                                                                              CLASSIFICATION:
                                                                                                                                                          APPLICATION NUMBER: US/08/947,823 FILING DATE: 09-OCT-1997
                                                                                                                                                                                                 OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97
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            REFERENCE/DOCKET NUMBER:
                       REGISTRATION NUMBER: 34,774
                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                           CITY: San Francisco
                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                     94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08947823
                                                                                                                                                                                                                                                                                             California
                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                 Milligan, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                          Williamson, Valeri
Kaloshian, Isgouhi
Yaghoobi, Jafar
                                                                                                                                                                                                                                                                                                                                                                                                                  Bodeau, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                              IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                       Floppy disk
INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.28;
                                                                            US 60/028,191
                                                                                                                  PCT/US97/18802
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           023070-070210US
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390 TTAAAATGTTTATAATTACATATTTATAATTAAAATGTTTATAATTACATATTTATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      646 GATTCGTACGATCTATCTAATGACTTTTTTTTTTTCTACCACGGTGGATGAAAGTTATAGT 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            586 TTTATTAATTTAAAAAACTCACAACTTGATCAGATAAAATTTCATAAACACTTTTACGATG 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGTTTATAATTAAATATTTTATAATTAAAATGTTTATAATTACATATTTATAATTAAA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTTAATGACGATGATAACAATTATATTTCTGACTTCTTAAAAACCCCCCTCTTACAAA 1004
                                                                                                           ATGTTTATAATT - - - - ACATATTTTATAATTAAAATGTTTATAATTACATATTTTATAA
                                                                                                                                                               AGAAACAAAAGCCATGAAGCTCATTGGTTAGTTTAAGCTTAATAAGAAGATTTTATTAAA 945
                                                                                                                                                                                                                                                                          AGTTTAATAAATAAAAGTATTAAAAAGGAGCATAACGAGGCAACAAAAGTAATGAACACGG 885
                                                                                                                                                                                                                                                                                                                                ACTATTAGCCAGAGACAATTGATTATAGATATATCCATTAATCCATGATATTTATGATAT 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
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  448
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Two Embarcadero Center, Eighth Floor PatentIn Release #1.0, Version #1.30 Townsend and Townsend and Crew LLF Procedures and Materials for Conferring Pest Resistance in Plants

TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 1:

TELEPHONE:

(415) 576-0200

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-641-638-651/c
                                                                                                                                       SOFTWARE: Pate
SEQ ID NO 651
LENGTH: 20674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 651, Application US/09641638 Patent No. 6432648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GENSET.051CP1
                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32533 ATTAAACAAATTTAAAATAAAATGTGTTGAATAGTTAATATTTTGTTCCTAAAAAACACTT 32592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32593
NAME/KEY: misc_feature
LOCATION: 1123..3123
OTHER INFORMATION: 5'regulatory region
NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32833 TTTCTTGATATATATATGATAAACTATTTAACAGGGGAAAATTTGACAAGAAAAA 32889
                                                                               FEATURE:
                                                                                                   ORGANISM: Homo sapiens
                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 51952 base pairs
TYPE: nucleic acid
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nilarity 47.68;
Conservative
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Pred. No. 0.23;
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NAME/KEY: allele
LOCATION: 1559
OTHER INFORMATION: 10-509-284
                                                                                                                NAME/KEY: allele
LOCATION: 2323
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 17555..20674
OTHER INFORMATION: 3'regulatory region
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OTHER INFORMATION: exon
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OTHER INFORMATION: exon
NAME/KEY: allele
LOCATION: 2832
                            OTHER INFORMATION: 10-512-318
                                         NAME/KEY: allele
LOCATION: 2623
                                                                        OTHER INFORMATION:
                                                                                                                                                                                             NAME/KEY: allele
                                                                                                                                                                                                        LOCATION: 1827
OTHER INFORMATION: 10-510-173
                                                                                                                                                                                                                                                        LOCATION: 1570
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                    NAME/KEY: allele
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LOCATION: 1182
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LOCATION: 1128
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OTHER INFORMATION: exon
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LOCATION: 13308..13429
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LOCATION: 12854..13023
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                                                                                      LOCATION: 2341
                                                                                                     NAME/KEY: allele
                                                                                                                                                                                                                                        NAME/KEY: allele
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NAME/KEY: allele
LOCATION: 6429
OTHER INFORMATION: 1
NAME/KEY: allele
LOCATION: 6467
OTHER INFORMATION: 1
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OTHER INFORMATION:
            NAME/KEY: allele
LOCATION: 8777
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LOCATION: 8703
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OTHER INFORMATION:
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LOCATION: 8608
OTHER INFORMATION:
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LOCATION: 6611
OTHER INFORMATION:
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LOCATION: 6484
OTHER INFORMATION:
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LOCATION: 6375
OTHER INFORMATION:
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OTHER INFORMATION: 10-343-339
NAME/KEY: allele
LOCATION: 5903
OTHER INFORMATION: 10-346-23
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LOCATION: 3802
OTHER INFORMATION:
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                                   OTHER INFORMATION:
                                                                                         NAME/KEY: allele
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LOCATION: 6338
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 4088
OTHER INFORMATION:
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LOCATION: 4062
OTHER INFORMATION:
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LOCATION: 6534
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LOCATION: 6183
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LOCATION: 6141
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LOCATION: 6019
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Best Local (
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                                                                                                                                                              GENERAL INFORMATION:
                                                                                             APPLICANT: Slade, Mart
APPLICANT: Chang, Andy
APPLICANT: Williams, K
TITLE OF INVENTION: IN
TITLE OF INVENTION: SI
NUMBER OF SEQUENCES: 1
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LOCATION:
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NAME/KEY: allele
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                    CORRESPONDENCE ADDRESS:
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                       COUNTRY: UZIP: 19103
                                                              STREET:
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                                            STATE:
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No. 5389526
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Chang, Andy C M
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Best Local Similarity
ZIP: 92bov
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION UMBER: US/08/487,826B
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APPLICANT:
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                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                          TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Feeney, Joanne Longo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US FILING DATE: 19920625 PRIOR APPLICATION DATA:
                                                                                                                                                                  STREET: 620 Newport Center Drive 16th Floor
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                                                                                                                                         COUNTRY:
                                                                                                                                                                                                 ADDRESSEE:
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SOFTWARE: Patent!
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5993827
                                                                                                                                                     California
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Chitnis, Chetan
Miller, Louis H.
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Wellems, Thoma
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SYSTEM: PC-DOS/MS-DOS
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BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE
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Pred. No. 0.19;
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                                                                                                                                                                                                                                                  Patent No. 5670367
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                 Sequence 14, Application US/08232463 Patent No. 5670367
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Best Local Similarity 47.3%;
Matches 169; Conservative
        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                        APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER,
APPLICANT: FALKNER, F. G
                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                      3629 AAGTATAATAATTAAATAATCATATAATAATAAAAACAATGTAAGAATCCAAGGTATA 3573
                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                 TITLE OF INVENTION:
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HYPOTHETICAL:
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 APPLICATION NUMBER:
                                                                                        COUNTRY: USA
ZIP: 22313-0299
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                                                                                                                                CITY: Alexandria
                                                                                                                                                STREET:
                                                                                                                                                            ADDRESSEE:
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TYPE: nucleic acid
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US/08/232,463
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Pred. No. 0.33;
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                                                                                                                                           Suite 500
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CLASSIFICATION: 435
IOR APPLICATION DATA:

APPLICATION NUMBER:

US/07/935,313

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                                                                                                                                    SEQ ID NO 3
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                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/08/213,419B
CURRENT FILING DATE: 1994-03-14
PRIOR APPLICATION NUMBER: US 07/870,506
PRIOR FILING DATE: 1992-04-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECAMUNICATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)833-4109
TELEX: 899149
                                                                                                                                                   SOFTWARE:
                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pair:
                                                                            TYPE: DNA ORGANISM: Plasmodium falciparum
                                     NAME/KEY: CDS
LOCATION: (24)
                       NAME/KEY:
                                                                       FEATURE
                                                                                                                   ENGTH: 6124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AACTTTAAAATAAATAAAATTTGAGTAAATGTGTTTTCTGACTATTGAGGGGCCAAAAA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
: (2407)..(2439)
: CDS
: (2598)..(3404)
                                                                                                                                                   PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                               Inselburg, J. et al.
PENTION: GENE ENCODING PROTEIN ANTIGENS OF PLASMODIUM FALCIPARUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.0%; Score 44; DB ilarity 7.8%; Pred. No. 0.35; Conservative 138; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-AUG-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/07867106 Patent No. 5389526
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 123;
                                                                  TELEPHONE: 215-568-31
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: (3580)..(3720)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (3850)..(5835)
                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Feeney, Joanne Longo
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1764
                                                   SEQUENCE CHARACTERISTICS:
                                                                                                       REFERENCE/DOCKET NUMBER: RITELECOMMUNICATION INFORMATION: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Macklewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1644 TATATAATAAAATTT 1630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1824 ATATATACATATTGTACATGTGTACATTTTTTTTTAAGAATAACAAGGGATTAGTTATCG 1765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
CITY: F
                                                                                                                                                         NAME: Feeney, Joanne Longo REGISTRATION NUMBER: 35,13
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 199206
                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
STRANDEDNESS:
                                 LENGTH:
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                  NUCLEIC ACID
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Chang, Andy C N
Williams, Keitl
                               5852 base pairs
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48.2%;
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Improved Plasmid Vectors for Cellular
Slime Moulds of the Genus Dictyostelium
                                                                                                                                                                                                                                                                                                                                        Release #1.0, Version #1.25
                                                                                                                                                      35, 134
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TOPOLOGY: 1

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US-07-991-867B-32

; Sequence 32, Application US/07991867B

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Best Local Similarity
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                              FILING DATE: 30-JAN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David
                                                                                                                                                                      SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                         MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NO. 54767
                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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FILING DATE: 12-DEC-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         968 TATATTTTCT 977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              848 AAAGGAGCATAACGAGGCAACAAAAGTAATGAACACGGAGAAACAAAAGCCATGAAGCTC 907
                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                         Gainesville
                                                                                                                                                                                                                                                       32606
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                                                                                                                                                                                                                                                                                             E: David R. Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                              PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                               Moyer, Richard W.
Hall, Richard L.
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2378..5038
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E: DNA (genomic)
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2378..5038
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                     JMBER: US 07/657,584
19-FEB-1991
                                                                                                                                                                                                                                                                                                                                          No. 5476781el Entomopoxvirus Expression System 66
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Pred. No. 0.41;
0; Mismatches 129;
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RESULT 15
US-08-107-755A-32
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                                                                                                                                                                                                                                                                                  Sequence 32, Applicati
Patent No. 5721352
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                         APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5721352el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 660 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
                                                                                                                                                                      ADDRESSEE: David R. Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                      1052 AAAGCCATTAGAAAGAGAAAGTGAGTGAGAGA 1083
                                                                                                                                                                                                                                                                                                                                                                                        448 GAGTTAAATATGGAATCAATACAAATAAAAGA 479
                                                                                                      ZIP:
                                                                                                                                    STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             388 TTAATAATATCTAAAAATAAATTTGGTAACTTTAATAATGTTTTTCCTATTAGTATAGTT 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         992 CCCCTCTTACAAACAGAAGCTCCCTTTTTCAGTAGAAGTCCGATTCCCAATCTTAAAGAC 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     932 AAGATTTTATTAAATTTTAATGACGATGATAACAATTATATTTTCTGACTTCTTTAAAAC 991
                                                                                                                COUNTRY:
                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  872 AGTAATGAACACGGAGAAACAAAAGCCATGAAGCTCATTGGTTAGTTTAAGCTTAATAAG 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268 TATAACAAAAATAGCAATATAAGTAATATTATACTACCACATTCTATAGAATTTTTAAAT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 AATATTATTAAATTTAAATTTTATAACAAATTAAAAATATAACATATTTAGATATATCT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         752 GATATTTATGATATAAATAGCTGTTAAACTATTTCAGCATCGCAGCTTTCTGCAACTTTT 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   692 ATGAAAGTTATAGTACTATTAGCCAGAGACAATTGATTATAGATATATCCATTAATCCAT 751
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                                                                                                    32606
                                                                                                                                               Gainesville
                                                                                                                                                                                                                                                                                                         <sup>2</sup>, Application US/08107755A
5721352
                                                                                                                                    Florida
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                                                                                                                                                    2421 N.W. 41st Street, Suite A-1
                                                                                                                U.S.A.
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Pred. No. 0.29;
""smatches 218;
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CLASSIFICATION:

FILING DATE: APPLICATION NUMBER:

19-AUG-1993

US/08/107,755A

Release #1.0, Version #1.25

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LENGTH: 660 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-107-755A-32
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Search completed: March 30, 2003, 08:58:03 Job time: 183.503 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/827,658
ETLING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US 07/657,584
ETLING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31/794
REFERENCE/DOCKET NUMBER: UF114.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8800
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 3.9%; Score 43.2; DB 1; Length 660; Best Local Similarity 44.4%; Pred. No. 0.29; Matches 174; Conservative 0; Mismatches 218; Indels 0;
                                                                           448 GAGTTAAATATGGAATCAATACAAATAAAAGA 479
                                                                                                                                                                                                                                  328
                                                                                                                                                                                                                                                                                                                                           872 AGTAATGAACACGGAGAAACAAAAGCCCATGAAGCTCATTGGTTAGTTTAAGCTTAATAAG 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 AATATTAATTTAAATTTTATAACAAAATTAAAAAATTAACATATTTAGATATATCT 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                752 GATATTTATGATATAAATAGCTGTTAAACTATTTCAGCATCGCAGCTTTCTGCAACTTTT 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCCTTTACAAACAGAAGCTCCCTTTTTCAGTAGAAGTCCGATTCCCAATCTTAAAAGAC 1051
                                                                                                                                                                                                                            AAAGCCATTAGAAAGAGAAAGTGAGTGAGAGA 1083
                                                                                                                                                                                                                                                                                                         TATAACAAAATAGCAATATAAGTAATATTATACTACCACATTCTATAGAATTTTTAAAT 327
                                                                                                                                                    TTAATAATATCTAAAAATAAATTTGGTAACTTTAATAATGTTTTTCCTATTAGTATAGTT 447
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0;

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OM nucleic - nucleic search, using sw model
                                                                                              GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Run on: March 30, 2003, 08:25:26; Search time 83.8565 Seconds (without alignments) 11172.915 Million cell updates/sec

Title: Perfect score: Sequence: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 US-09-502-426A-1_COPY_2102_3202 1101 1 aatctacaaattattaatat.....gagagagagaaactagctcc 1101

Scoring table:

Searched:

Total number of hits satisfying chosen parameters:

574371 seqs, 425486471 residues

1148742

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Published_Applications_NA: * /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

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) × F	Score	Match	Query Match Length	8	ID	Description
1	54.4	4.9	516	10	US-09-960-352-5785	Sequence 5785, Ap
N	53.2	4.8	431	10	US-09-960-352-5558	
ω	52.2	4.7	377	10	US-09-960-352-7419	Sequence 7419, Ap
4	52.2	4.7	446	10	US-09-960-352-3400	Sequence 3400, Ap
5	49.2	4.5	6265	10	US-09-129-112-3	Sequence 3, Appli
6	48.6	4.4	53332	9	US-10-224-562-3	Sequence 3, Appli
7	48.6	4.4	53332	10	US-09-801-861-3	Sequence 3, Appli
œ	48.4	4.4	406	10	US-09-960-352-10265	Sequence 10265, A
9	47.8	4.3	294	10	US-09-960-352-4637	Sequence 4637, Ap
0	47	4.3	419	10	US-09-960-352-11234	_
-	46.2	4.2	1713	9	US-09-938-842A-4756	Sequence 4756, Ap
N	46	4.2	32463	9	US-09-996-956-5	Sequence 5, Appli
ω	45.8	4.2	428	10	US-09-960-352-573	Sequence 573, App
4	45.6	4.1	1109	9	US-09-938-842A-3333	Sequence 3333, Ap
G	45	4.1	413	10	US-09-960-352-2919	Ψ
σ	44.2	4.0	344	10	US-09-960-352-1036	Sequence 1036, Ap
7	44.2	4.0	4187	9	US-10-072-349-252	Sequence 252, App
œ	44.2	4.0	4187	10	US-09-764-855-252	Sequence 252, App
9	44	4.0	376	10	US-09-960-352-5087	Sequence 5087, Ap

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US-09-938-842A-4902 US-09-754-853A-2	US-09-115-453-102 US-09-938-842A-3089	US-09-822-827-102	US-09-030-606-102	US-09-780-669-102	US-09-759-143-102	US-09-895-814-102	US-09-895-793-102	US-10-012-896-102	US-09-232-880-102	US-09-960-352-10262	US-09-969-373-937	US-09-960-352-11218	US-09-803-719-1436	US-09-938-842A-4090	US-09-960-352-7907	US-09-790-988-1	US-09-960-352-4584	US-09-938-842A-4975	US-09-960-352-4582	US-09-938-842A-3251	US-09-960-352-12911	US-09-790-988-1	US-09-754-853A-4
Sequence 2, Appli	102,	102			~	Sequence 102, App	Sequence 102, App	Sequence 102, App	Sequence 102, App	Sequence 10262, A	Sequence 937, App	Sequence 11218, A	Sequence 1436, Ap	Sequence 4090, Ap	Sequence 7907, Ap	Sequence 1, Appli	Sequence 4584, Ap	Sequence 4975, Ap	Sequence 4582, Ap	Sequence 3251, Ap	Sequence 12911, A	Sequence 1, Appli	Sequence 4, Appli

ALIGNMENTS

ОУ ОУ ОУ ОУ	Que Bes Mat	RESULT 1 US-09-96 Sequen Peten Peten APPLL APPL
5 TACAAATTATTAATATTTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAAA	Query Match 4.9%; Score 54.4; DB 10; Length 516; Best Local Similarity 48.7%; Pred. No. 0.09; Matches 148; Conservative 0; Mismatches 156; Indels 0; Ga	US-09-960-352-5785/c US-09-960-352-5785/c US-09-960-352-5785/c Sequence 5785, Application US/09960352 Patent NO. US20020137139A1 GENERAL INFORMATION: APPLICANT: Warren, Wesley C. APPLICANT: Byatt, John C. APPLICANT: Byatt, John C. APPLICANT: Mathialagan, Nagappan TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE REFERENCE: 16511.006/37-21(10298)C CURRENT APPLICATION NUMBER: US/09/960,352 CURRENT FILING DATE: 2001-09-24 SEQ ID NO 5785 LENGTH: 516 TYPE: DNA ORGANISM: Bos taurus FEATURE: NAME/KEY: unsure LOCATION: (76),(90) OTHER INFORMATION: unsure at all n locations OTHER INFORMATION: Clone ID: 25-LIB3057-018-01-K1-G1
64 401 124 124 341 184 281	Gaps	H LAC
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US-09-960-352-7419/c

: Sequence 7419, Application US/09960352

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; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone
US-09-960-352-5558
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US-09-960-352-5558/c
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 15511.006/37-21(10298)C
CURRENT EPPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001.09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Warren, Wesley
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EQ ID NO 5558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 431
                                                                                                                                                                                     189
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                                                                                                                                                                                                                                                                                                                                                                                           CAAATTATAAATAAACCAACACGCTC 44
                                                                                                      TTCGGTAATAATCTAATAACTCTGTC 401
                                                                                                                                                        TCTGACTATTGAGGGGCAAAAAAAGACAATGCCAAAAGTCTACGGGTTTGACTGTCCAG 375
                                                                                                                                                                                  AAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAATTGGGACAAC 255
                                                                                                                                                                                                                                                                                                               TGGAAGTAGTAATACATTAAGCAAATTTTAAAAAATTATATAAGCCTATACGCGCTCA 195
                                                                                                                                Tao, Nengbing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
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GENERAL INFORMATION:

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APPLICANT: Byatt, John C.

APPLICANT: Mathialagan, Nagappan

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND INVENTION: MUSCLE AND FAT DEPOSITION

FILE REFERENCE: 16511.006/37-21(10298)C

CURRENT FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 15112

SEQ ID NO 7419
LENGTH: 377
TYPE: DNA
ORGANTON:
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; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 32-LIB3057-025-Q1-K1-H11
US-09-960-352-7419

                                                                    US-09-960-352-3400
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                                                                                                                                                                                                                                                                                                                                              Sequence 3400, Application Patent No. US20020137139A1
                                                                                                                                                 SEQ ID NO 3400
                                                                                                                                                                                                                                                                                                                             GENERAL
     Best Local Sin
Matches 165;
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Best Local
                                 Query Match
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                                                                                                                                                             APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10299)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILLING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
                                                                                                                                                                                                                                                                                          APPLICANT: Warren,
APPLICANT: Tao, No
                                                                       LENGTH: 446
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 15-LIB3058-052-Q1-K1-D11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGATGAAAGTTATAGTACTATTAGCCAGAGACAATTGATTATAGATATATCCATTAATCC 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGTTTTTAATTTAAGAGTTTAATAAATAAAAGTATTAAAAGGAGCATAACGAGGCAACA 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161;
                     Similarity
                                                                                                                                                                                                                                                                                            Tao, Nengbing
     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.5%;
                  4.78;
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 Score 52.2; Di
Pred. No. 0.23
0; Mismatches
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Pred. No. 0.22;
0; Mismatches 163;
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                  . 23;
                                   DB
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     188;
   Indels
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 6265
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                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/129,112
CURRENT FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: US 08/907,226
PRIOR FILING DATE: 1997-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Etzler, Marilynn E.
APPLICANT: Murphy, Judith B.
APPLICANT: The Regents of the University of California
TITLE OF INVERTION: A NO. US2002001995Al Factor Binding Protein From Legume Roots
FILE REFERENCE: 023070-079810US
                                                                                                                                                        NAME/KEY: exon
LOCATION: (169
                                                                                                                                                                                                                                                                     NAME/KEY: exon
LOCATION: (633)..(944)
NAME/KEY: intron
2877 TCTTTTTTTTTTTTTTTTTTATTGAAAATGTTTTGAAATATTGTCAAATATTAATAATAGTGA 2818
                                          2936 TATTTTATAGTGTTTTACTATTCAAATAAACATAATGCAGATATGAAGTTTACTG-AACT 2878
                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: genomic sequence of NBP46
                                                                                                                                                                                                                                                                                                                            ORGANISM: Dolichos biflorus
                                                                                                                                                                                                                                                      NAME/KEY: exon
               Local Simi
hes 173;
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Similarity 53.1%;
73; Conservative
                                                                                                                                                                       (1617)..(1697)
                                                                                                                                                                                                                                                             (945)..(1022)
                                                                                                                                                                                           (1560)..(1616)
                                                                                                                                                                                                                   (1152)..(1559)
                                                                                                                                                                                                                                       (1023)..(1151)
                                                                                        Score 49.2; DB 10;
Pred. No. 2.4;
0; Mismatches 148;
                                                                                        Indels
                                                                                                             Length 6265;
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                                                                                       Gaps
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Sequence 3, Application US/09801861
Patent No. US20020119544A1
GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN
TITLE OF INVENTION: ACID MOLECULES
TITLE OF INVENTION: THEREOF
                                                                                                        RESULT 7
US-09-801-861-3/c
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TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILLE REFERENCE: CL00109BDIV
CURRENT APPLICATION NUMBER: US/10/224,562
CURRENT FILING DATE: 2002-08-21
NUMBER OF SEQ ID NOS: 10
SOFTMARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3
SEQ ID NO 3
LENGTH: 53332
TYPE: DNA
ORGANISM: Homo Sapiens
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FILE REFERENCE:
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                                                                                                                                                                                                      31551
                                                                                                                                                                           287 AATAAATAAAAATTTGAGTAAAT 309
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                                                                                                                                                                                                                                                            TCAAAGTATGTTATCTAGTAGGTGTAATTAATA--ATGCATGGTGCGATTCAGAATTGGG 250
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 YAN, Chunhua et al.
VENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
VENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
CL001098
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49.0%; Pred. No. 7;
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SOFTWARE: SEQ ID NO 3

FastSEQ for Windows Version 4.0

NUMBER OF SEQ ID

NOS:

CURRENT APPLICATION NUMBER: US/O CURRENT FILING DATE: 2001-03-09

us/09/801,861

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                                                                                                                                                                                                                         ; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 44-LIB3058-038-Q1-K1-C12
US-09-960-352-10265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Human
US-09-801-861-3
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                                                                                                                                                                                                                                                                               SEQ ID NO 10265
LENGTH: 406
                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10265, Application US/09960352 Patent No. US20020137139A1
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Best Local Similarity
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APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE ACID FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAACTATTTTGTTGTGGAATGGAAGTTAGTAATATACATTAAGCAAATTTTTAAAAAATTAT 176
                          ATTTTTTTTATTTTAAATTATGTGTTTCATTTTAGTATTTATATTAAATTATTCCTTAA
|||| ||||| || || || || || AATATATAAATATATAAAATATATA 31409
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                                                     AATAAATAAAATTTGAGTAAAT 309
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                                                                                                                                                                   Conservative
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                                                                                                                                                                               Score 48.4;
Pred. No. 1.
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Pred. No. 7
                                                                                                                                                                  Mismatches
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; OTHER INFORMATION: Clone US-09-960-352-11234
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; OTHER INFORMATION: Clone ID: 20-LIB3058-054-Q1-K1-E11
US-09-960-352-4637
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                                                           APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathalagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION /
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,3552
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 11334
LENGTH: 419
                                                                                                                                                                                                                                                    APPLICANT: Warren,
                                                                                                                                                                                                                                                                                       Sequence 11234, Application Patent No. US20020137139A1
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LENGTH: 294
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APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathalagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND FITE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
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                             ORGANISM: Bos taurus
                                               TYPE: DNA
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les 115; Conserv
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              ID: 48-LIB3058-052-Q1-K1-D8
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Pred. No. 1.
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                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-4756
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US-09-938-842A-4756
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                                                                                                                                                                      Query Match
Best Local Similarity
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SEQ ID NO 4756
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CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                              LENGTH: 1713
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                                                                                                         251
                                                                                                                        71 AACTTCCAAATTTTTTTTTTTTTTATGGAACAAGAAATAACAGATAGAAAACTATTTTGTTG 130
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                                                                                                                                                           Conservative
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                                                                                                                                                         Score 46.2; DB 9;
Pred. No. 5.7;
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; TYPE: DNA
; ORGANISM: HOMO
US-09-996-956-5
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Best Local Similarity
Matches 142; Conserv
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SEQ ID NO 5
LENGTH: 32463
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                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                             Sequence 573, Application US/09960352 Patent No. US20020137139A1
APPLICANT: Byatt, John G.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLERIC ACID AND OTHER MOLECULES
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 15511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
                                                                                                                              APPLICANT: Warren, Wesley C. APPLICANT: Tao, Nengbing APPLICANT: Byatt, John C. APPLICANT: Mathialagan, Nag
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CURRENT FILING DATE: 2001-11-30
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ilarity 47.08;
Conservative
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CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION UNMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION UNMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 3333
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LENGTH: 428
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                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
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OTHER INFORMATION: Clone ID: 03-LIB3058-031-Q1-K1-A11
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                                                                                                                         Local Similarity
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                                                                          1 AATCTACAAATTATTAATATTTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAATTT
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Zhu, Tong
                                                                                                          Conservative
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Pred. No. 6.3;
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; NUMBER OF SEQ ID NOS: 15112

; SEQ ID NO 2919

; LENGTH: 413

; TYPE: DNA

; ORGANISM: Bos taurus

; OTHER INFORMATION: Clone ID: 13-LIB3058-032-Q1-K1-D1

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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
APPLICANT: MICLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION INTILE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 138; Conserv
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                                                                                                                                                                                       483 TTAATATTAATGAATAGTTCATAT 460
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                                                                                                                                                                                                                                                                                    TTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGCCT
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AAACAAGAAAAAAAAAATATTAATAAAAATAGAAAAAGAAAATAAGTAAAA
                                                                                           ATACGCGCTCAAAGTATGTTATCTAGTAGGTGTGAATTAATAATGCATGGTGCGATTCAGA
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Pred. No. 5.7;
0; Mismatches 155; Indels
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Search completed: March Job time: 210.856 secs

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Minimum
Maximum
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Perfect score:
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ALIGNMENTS

REFERENCE AUTHORS KEYWORDS SOURCE ORGANISM ACCESSION VERSION LOCUS DEFINITION RESULT 1 BH811044/c COMMENT TITLE JOURNAL BH811044 148 bp DNA linear GSS 02-MAY-200 SALK_057128 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_057128, DNA sequence. Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379 Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Ga, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Zimmerman, J. and Ecker, J.R.

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. BH811044 BH811044.1 This is single pass sequence recovered from the left border of Arabidopsis Genome Unpublished (2001) thale cress. GSS (bases 1 to 148) ecker@salk.edu GI:20388862 Cheuk, R., Gadrinab 02-MAY-2002 Shinn, P

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                                                                                                                   Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer 2uechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone T3A5. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the GPI for Plant Genomics program designated 'GABI'. Information on line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosso,M., Strizhov,N., L1,Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
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                                                             availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
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- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster
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/strain="Columbia 0"
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Drosophila melanogaster
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Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

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 Submitted (23-JUL-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail: - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was collaboration with the European Drosophila
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/db_xref="taxon:7227"
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segref@genoscope.cns.fr
carried out as part of a Genome Project (EDGP) -
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                        ATAAAAAAWAAAWAWWWAAAAAATWWTAAATATAAWTTAAATNCATAAAACAAAAAWAA 728
                                                                                                                                TTTAAGCTTAATAAGAAGATTTTATTAAATTTTAATGACGATGATAACAATTATATTTTC 976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pBeloBAC11.
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/note="end : T7"
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/db_xref-"taxon:727"
/clone-"BACN15M24"
/clone_lib-"DrosBAC"
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RESULT 5
CNSOODKY
LOCUS
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ORGANISM
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VERSION
 REFERENCE
                                                                                                   KEYWORDS
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         Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                             Drosophila melanogaster genome sur
BACR27A24 of RPCI-98 library from
fly), genomic survey sequence.
 Ephydroidea;
1 (bases 1 )
                                                                                                                                    AL071865
                                                                               Drosophila melanogaster.
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928)
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rom Drosophila melanogaster
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end of BAC #
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RESULT 6
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TITLE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACAAATTATTAATATTTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAATTTTGTT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 1809enic strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP 191 91006 EVRY codex FRANCE (E-mail: seqrefegenoscope.cr - Web: www.genoscope.cns.fr)

Determination of this BACE sequence was carried out as part collaboration with the Berkeley Drosophila Genome Project (BDC The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACS. For further information
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Direct Submission

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fi
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                              Drosophila melanogaster genome survey sequence SP6 end of BACN15C02 of DrosBAC library from Drosophila melanogaster
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                                                                                                                        AL106335.1 GI:5621422
                                                                                 Drosophila melanogaster.
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                                                                                                                                                            genomic survey sequence.
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/note="end : T7"
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/db_xref="taxon:7227"
/clone="BACR27A24"
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Best Local
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                                                AUTHORS
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                                                 Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Pphydroidea; Drosophilidae; Drosophila.
                                                                                                                                                             GSS.
                                                                                                                                                                                         fly), gen
AL061936
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Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Submitted (02-JUN-1999)
BP 191 91006 EVRY cedex
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BACR05N11 of RPCI-98 library from
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                                 Direct Submission
                                                Genoscope
                                                                                                                                         Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                        genomic survey sequence.
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/plasmid="pBeloBAC11"
/note="end : SP6"
a 193 c 54 g '
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/db_xref="taxon:7227"
/clone="BACN15C02"
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37.2%;
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Pred. No. 0.0061;
Genoscope - FRANCE (
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National de Sequencage 
segref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                  ATTATTTWTTATT 874
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                                       Drosophila melanogaster.
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Neoptera; Endopterygota; Drosophila.
Ephydroidea; Drosophilidae; Drosophila.
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AL078714
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BACR48P19 of RPCI-98 library from
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/db_xref="taxon:7227"
/clone="BARROSAII"
/clone_lib="RPCI-98"
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SOURCE

ORGANISM

GSS. Drosophila melanogaster. Drosophila melanogaster Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Eukaryota; Miscomorpha;

KEYWORDS VERSION ACCESSION CNS00EVL/c

DEFINITION **FOCUS** RESULT 9

CNSODEVL 1101 bp DNA linear GSS 04-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC: BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit

fly), genomic survey sequence. AL069706.1 GI:4949849

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                                                                TTAATAAGAAGATTTTATTAAATTTTAATGACGATGATAACAATTATATTTTCTGA
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                                                                                                                                        KWDGAKKATKTKKKDKKAAWAAADKKDRKKGGKKKGKKGKKGKKGKKKKKKKKKGKGGWGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

    Web: www.genoscope.cns.fr)
    Determination of this BAC-end sequence was carried out as

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/db_xref="taxon:7227"
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- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila constructing a physical map of the Drosophila recommendation of the BDGP is constructing a physical map of the Drosophila recommendation of the BDGP is constructed by the BDGP is constructed as the BDGP is constructed by the BDGP 
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns
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                                   ACGATGATAACAATTATATTTTCTGACTTCTTTAAAACCCCCTCTTACAAA
                                                                                                   AAAANTTTKRRDKRTTTTTTDRTTTWWTTAAAAAAWTTWTTAWTTTTTATTATAAAWA
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                                                                                                                                                                          AAGCCATGAAGCTCATTGGTTAGTTTAAGCTTAATAAGAAGATTTTATTAAATTTTAATG 953
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This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Welssenbach, J.
Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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Roest-Crollius, H., Jaillo
Bouneau, L., Billault, A.,
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Tetraodon nigroviridis.
Tetraodon nigroviridis
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
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/note="Genoscope sequence ID : C0AG225BH02LP1-end : T7"
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                                                         Drosophila melanogaster genome sur
BACR24D09 of RPCI-98 library from

    Web: www.genoscope.cns.fr)
    Determination of this BAC-end sequence was carried out as collaboration with the Berkeley Drosophila Genome Project

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                                                                                                        CNS00BO1
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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                   fly), genomic survey sequence.
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Ephydroidea; Drosophilidae;.Drosophila.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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Location/Qualifiers
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
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The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Ephydroidea; Drosophilidae; Drosophila.
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGTGTTTTCTGACTATTGAGGGGCAAAAAAAAAAGACAATGCCAAAAGTCTACGGGTTTGA
                                                                                  AGAAACTTCCAAATTTTTTTTTTTTTATGGAACAAGAAATAACAGATAGAAAACTATTTTG 127
                                                                                                                   WTTWTAWWATWWAWWTATAWATAWAATAWAAWAWAWATAAATAWATAWATWAAAWAWA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/note="end : T7"
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/db_xref="taxon:7227"
/clone="BACR29B23"
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186 TACGCGCTCAAAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAA 245
                                                                                                                                                         y Match 5.7%;
Local Similarity 44.0%;
hes 153; Conservative 18
                                                                                                                                                                                                                                                           947 TTATTAAAWTWTATWWATTWATTWWAWTWTATAWTTWTA 985
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Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
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Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouncau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetier, F., Saurin, W. and Weissenbach, J.

Human gene number estimate provided by genome wide analysis using Tetracodon nigroviridis DNA sequence
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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GSS; genome survey sequence.
Tetraodon nigroviridis.
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Search completed: March 30, 2003, 08:52:57 Job time: 1451.66 secs

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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SUMMARIES

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ALIGNMENTS

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linear PI BAC clone T3A5.

PLN 26-JAN-2000

	AUTHORS	REFERENCE				ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	ATT3A5/c	RESULT 1	
Calanouhat M	Bloecker, H., Mewes, H.W., Lemcke, K.,	1 (bases 1 to 84196)	Rosidae; eurosids II; Brassicales; B	Spermatophyta; Magnoliophyta; eudico	Eukaryota; Viridiplantae; Streptophy		Arabidopsis thaliana.	•	AL132979.2 GI:6782244	AL132979	Arabidopsis thaliana DN	ATT3A5 84196 bp E			

Salanoupat, M. ophyta; Embryophyta; Tracheophyta; dicotyledons; core eudicots; s; Brassicaceae; Arabidopsis. (., Mayer, K.F.X., Quetler, F. and

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number of results predicted by chance

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12804. .1
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Iefvdleenngddretetswiyddlnkseesnnmdsssvavedvesrrrlrkslhetv
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                                                                                                                                                thaliana"
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(ICKI), Arabidopsis thaliana, EMBL:ATU94772_1"
                                                                                                                                                                                                                                                                              13125. .13197
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/gene="T3A5.10"
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                                                                                                                    /codon_start=1
                                                                                                                                                                   'note="similarity
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/ COUCH_S CALL-1
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TLFVLDSWQQNSIFSAQDEAKKFTENLMAKH_MSMDPGEEETEGLKKEYVTFMKGYVS
APLNLDGTAYHKALQSRATILKFIERKMEERKLDIKEEDQEEETEGLKKEYTEDEAEMSKSDH
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EELREEHLEIARAKKELGESELNWDDYKKMDFTQCVINETLIGNVVRFLHRKALKDV
RYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLENPWRQOQNNGASSGSGSFSTWGN
RYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLENPWRQOQNNGASSGSGSFSTWGN
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PSTGTFTLFGGGFSDFFQVTNDFGFHFPLEHHQNAAVASEEFDSDEWMESLIKGGDAS
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RSLNPRIVTLGSYEVSUNTUSTANTVUNSLRFYSAVFESLEPVKPSNYAVSQAKLLLM
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VXMCTYTTUSTANTVUNSLASH
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27478. .27570,27723. .:
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/gene="T3A5.30"
complement(18303. .19931)
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QVADTR"
                                               /number=6
                                                                    complement (28136.
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ERIHKLREKGVEKAABDLKKYDPNNDPNATGDPYKTLFVSRLMYESSESKIKREFES
YGPIKNYLLYTDQLTNNFKGYAFIEYMHTRDMKAAYKQADGQKIDGRRVLYDVERGRT
YGPIKNYLTYDQLTNNFKGYAFIEYMHTRDMKAAYKQADGQKIDGRRVLYDVERGRT
RSRELSHEQFRERSKDRFEDIVHHTRDMKDAYKGADGQKTGGKERE
RSRELSHEQFRERSKDRFEDIVHHTRDMCDGGRTGQSEEPSRPXEEREKSREKKER
GRDRTSRDHNCDTSRKKERDYEGGEFUHEGGGRSRENDRDRTRDRDRTRDRDR
GRDRTSRDHRDRSRKKERDYEGGEFUHEGGGRSRERDRTRGFYEDDQGD
COMPLEMENT (38307. 38796)
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complement(40243. .40336)
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/note="Contains Eukaryotic putative RNA-binding region RNP-1 signature AA179-186"
/codon_start=1
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/gene="T3A5.50"
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Pred. No. 0;
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TATCCTAAGGGTAATTTTGGAAATCCCAATTTAAACCGATTGAGACCGTACCGGACTTCC
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                                                                                     TAAATACATTATGAACCAATAATAGTTGGTGAATTCAAATATCTCCCATTAATATTTTTG
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                                               GGGTTTGACTGTCCAGTTCGGTAATAATCTAATAACTCTGTCTTTGACCGCACGCTCGTG
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Direct Submission
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                 Submitted (22-JAN-1998) Plant Tucson, AZ 85721, USA
                                                                                                       The DWF4 gene of Arabidopsis encodes a mediates multiple 22alpha-hydroxylation
                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

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                                                                         GGCAAAAAAAAAGACAATGCCAAAAGTCTACGGGTTTTGACTGTCCAGTTCGGGTAATAATCT
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/product="steroid 22-alpha-hydroxylase"
/protein_id="AACO5093.1"
/db_xref="G1:2935342"
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GWPFLGETIGYLKPYTATTLGDEWQOHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQ
REGRLFECSYPRSIGGILGKWSMLVLVGDMHRDMRSISLNFLSHARLRFILLKDVERH
TLFVLDSWQQNSIFSAQDEAKKETFHIMAKHLMSMDF0GEETEQVKTEDEAEMSKSDH
FLVLDSWQQNSIFSAQDEAKKETFHIMAKHLMSMDF0GEETEQVKTEDEAEMSKSDH
VRKQRTDDDLLGWVLKHSNLSFEQILDLILSLLFAGHETSVAAIALAFFLQACPKAV
EELREBELEIAAAKKELGESELIWNDDYKKMDFTQCVINETLRGUNVVRELHRKAILDV
RYKGYDIPSGWKVLPVISAVHLDNSRYDQNLFNPWRQQQNNGASSGSGSFSTWGN
NYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAEDDQPFAFPFVDFPNGLPIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="brassinosteroid biosynthetic enzyme"
/note="member of the cytochrome P450 superfamily; cyp90Bl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="steroid 22-alpha-hydroxylase"
join(1133. 1353,1434. .1758,1844. .1996,2095.
2562. .8654,2746. .2824,2931. .3040,3795. .404
/gene="DWF4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /allele="dwf4-1; dwf4-2; dwf4-3; dwf4-4"
990. .1055
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2562. <u>2654,</u>2746. .2824,2931. .3040,3795. .4398)
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/chromosome="III"
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/strain="Ws-2"
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                                                                          AGAAGATTTTATTAAATTTTAATGACGATGATAACAATTATTTTTCTGACTTCTTTAAA
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JOURNAL REFERENCE AUTHORS JOURNAL

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tagged site. AL844732

AL844732
191 bp
Arabidopsis thaliana transposon

insertion DNA

linear STS 25-JUL-2002 STS SM_3.29533, sequence

AL844732

2 (Dases J.H. Clarke J.H. John Innes Centre, Colney Direct Submission Submitted (25-JUL-2002) Clarke J.H. John Innes Centre, Colney Lane, Norwich, NR4 7UJ, UK AT denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, GT a graph dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, SM a defective suppressor mutator dissociation transposon, SM a defective from the 3'end of the Murphy, G., Unpublished Clarke, J.H., Bowles, B., Murphy, G., Langham, S., I Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. Carter,J., Hart,D., McCullagh,B.,
LeGrys,C., Jones,J.D.G. and Bevan, LeGrys,C., Bevan, M. gene

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                                                                                                                 94304, USA
On Apr 2, 1999 this sequence version replaced gi:4337172.
NOTE: This is a 'working draft' sequence. It currently
consists of 3 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

**R642. Contig of 58642 bp in length
                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 104992)
Hyman,R.W., Qin,F., Fung,E.L., Conway,A.B. and Davis,R.W.
Direct Submission
Submitted (21-AUG-1998) Stanford DNA Sequencing and Technology
Center, Stanford University, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hyman, R.W., Fung, E.L., Qin, F., Tamaki, T., and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 104992)
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Plasmodium falciparum chromosome 12,
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seed stock requests: http://nasc.nott.ac.uk/ NASC stock
Location/Qualifiers
1. .104992
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37 c 28 g 56 t
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/db_xref="taxon:3702"
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                                58642: contig of 58642 bp in length
58842: gap of unknown length
91011: contig of 32169 bp in length
91211: gap of unknown length
104992: contig of 13781 bp in length
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Pred. No. 3.8e-16;
0; Mismatches 2;
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2, *** SEQUENCING IN PROGRESS
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                           CTCGACCCTTAAAATACGATTTTACAGCGTCACTAGTTGAGATTACTAGCATAAAGCATA 1064
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                                   AATTTTTGAAAAATGTTATAATTTCTAACAATATTATTAAAATATGATGCCTATAATGTA 2000
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                          108 ATAATTAAATATTAAAATTCATTTAAAATATTTACA-AGTAATTAATTATCTTTACATTG 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Aug 12, 2000 this sequence version replaced g1:8810447, *NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (19-FEB-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. I (bases 1 to 169546) (Din,F., Rowley,D., Mao,J., Tamaki,T., Kurdi,O.B., Conway,A.B. and Davis,R.W. Plasmodium falciparum 3D7 chromosome 12
                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hyman, R.W., Qin, F., Fung, E.L., Conway, A.B. and Davis, R.W
                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Plasmodium falciparum chromosome 12
PROGRESS ***, 2 unordered pieces.
AC004157
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                                                                      Conservative
                                                                                                                                                                                                                                                                                23467
23667
                                                                                                                                                                   /clone="PFYAC293"
/clone="3D7"
                                                                                                                                                                                            /organism="Plasmodium
/db_xref="taxon:5833"
/chromosome="12"
                                                                                                                                                                                                                                           1. .16954
                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                             15381 c 15705 g
                                                                                   4.28;
44.78;
                                                                                                                                                                                                                                                                  23466: contig of 23466 bp in length
23666: gap of unknown length
169546: contig of 145880 bp in length
                                                               Score 133.2; DB 2;
Pred. No. 1.5e-10;
0; Mismatches 1248;
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                                                                                             Length 169546;
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TAACATATCCATATATGGGTATGCTATACCTTTCACGTATGCTATACTAGA	AATCAATTAGTGGTCAACATATACATAATTCCTTACAGAAAAAAAA	GAAAATTTTGGAATTACCGGTTGTTATGTAAATATAGATTTAGTGGTAAACAATATGTT	S AAGGACCCGTTCAAGCTATTTATACAAAGTTACAAACTGAAATATGGTTGAAATCCTTTA 1124 	CTCGACCCTTAAAATACGATTTACAGCGTCACTAGTTGAGATTACTAGCATAAAGCATA			S TCAATATTATGTTCCAGGTATTTGCATAATCTTCTGTTTAAAGCATATTTTGTCTTTCTT	is tggatattcgttaaaatttgcgataacgattgtgaaaaatattttatttgttagctgatc 824 	TGGAATAATGGTCCCTGCCAGCTTTCTCTCACAATGCAATATGGACCCTATTTGGATTTTC 764	5 TGACCCATGGAGTATGTGAATAATTATCAAAGAGAATAAGAGATGACAACCAAAAGGTTG 704	35 CAGCAAATTATTAACAAGAGTATTGAGAAAAAACCGAAAATAAGAAAAGGGAAAGAGTAG 644 	S ACGAGTGTGAATATCCGTTTATCGATCACTCCAATCATGATTATGATTCTTGTGCTAATC 584	5 ATGAAGATTTTCTTACCAATTAAAATTTCGAATTCATATCTCTTGATTATTAATTA)5 TTTTTGGTTCTGGATTAGGTTTATTTGATCATAATTACATGCATCATTTCTTTGATTACT 464 	6 TCGTTATGACCCCCAAAAAAAAAAAAAAAAAAAAACCAAACCA-AACAAACCCCCC	16 TCTTTTGTTATATGTATATGAGTAAATCAAAAAGAGTATTGATTG	27 AATAATAAAGGAAATAARCGATTGCCATTTGGGTTGGAT-TACACAGTTAAGTTTTTGTGTT 285 	7 TATTGTTATAACAAAATATCTATCTTTGGTATATGAGAAAATATGGGGTTTGGAATTTAT 226
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2297 AAGTATGTTATCTAGTAGGTGTGAATTAATGATGATGGTGCGATTCAGAATTGGGACAAC 2356	2237 TGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAGCCCTATACGCGCTCA 2296	2177 CCAAATTTTTTTTTTTATGGAACAAGAAATAACAGATAGAAAACTATTTTGTTGTGGGAA 2236 	2117 AATATTTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAATTTTGTTAACAGAAACTT 2176 	2061 AATAGTIGGTGAATTCAAATATCTCCATTAATATTTTIGAAATCTACAAATTATT 2116	2001 TTTCCTATGTTCTTAAAATATTTTTTTTTATATTTAGTTATAAATACATTATGAACCAAT 2060 	1941 AATTITTGAAAAATGTTATAATTTCTAACAATATTATTAAAATATGATGCCTATAATGTA 2000 	1881 AATTCAATGCTACTATCAATAGAAGAAACAGCTGAGTATTACATTTTAATTTTAAAGACAA 1940 	1824 ATAATGACAGCCTCTACAACTGTGATAGTCAATTTTTTCTGCAAATATTAAATTAGG 1880 	1764 TAATTTTTTGAAAATGTAACCCTTTTACTCATAGATTAATTA		ACATACTTTGGATGTTTAAACTTAATCTTGTTTCTTCCTACGGTATAAATATTAATCATC	1596 TGTAACATTACAATATTTATATTAGATACTAGTATGTGATTATTCCAAAT 1645 	1536 GCTTTCTTTAATGCATCCTTTAACATATTTATTGTTAGTTGGAATTTAATAAGAGCGAACT 1595	1476 CTTTTGGGTTACAGTTTCGAAGTCCTCTACAAGCGTGTAACCATCTGCAACTATTAAATT 1535				

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1245 TAACATATCCATATATGGGTATGCTATACCT-----TTCACGTATGC

1125 GAAAATTTTGGAATTACCGGTTGTTATGTAAATATAGATTTAGTGGTAAAC

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KEYWORDS
SOURCE
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                                 74559 AAAATAAAAATAATAATTATTATTATATATATATATTAATTAATTAAATTAAATTATTAT 74500
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TAATAATAAAGGAAATAATCGATTCCATTTGGTTGGATTACACAGTTAAGTTTTTGTGTT
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Submitted (21-AUG-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto,
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Plasmodium falciparum chromosome 12,
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* NOTE: This is a "working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Plasmodium falciparum"
/db_xref="taxon:5833"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58642: contig of 58642 bp in length
58842: gap of unknown length
91011: contig of 32169 bp in length
91211: gap of unknown length
104992: contig of 13781 bp in length
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                                                                                                                                                                                                                                                                                                                      Score 130.8; DB 2; Pred. No. 3.8e-10;
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                                                  AGACTAAAGAA-----TAGTTATGTGATGTCGATAAATGAAATTCACACGCGTGGTAAT 1348
                                                                                                                                                         TAAGAGAAGTTAACATATCCATATATGGGTATGCTATACCTTTCACGTATGCTATACTAG
                                                                                                                                                                                                           CCTTTAGAAAATTTTGGAATTACCGGTTGTTATGTAAATATAGATTTAGTGGTAAACAAA 1178
                                                                                                                                                                                                                                                                                                               AGCATAAAGGACCCGTTCAAGCTATTTATACAAAGTTACAAACTGAATATAGCTTGAAAT 1118
                                                                                                                                                                                                                                                                                                                                                                 ACTGGACTCGACCCTTAAAATACGATTTTACAGCGTCACTAGTTGAGATTACTAGCATAA 1058
                                                                                                                                                                                                                                                                                                                                                                                                                     TATCACAAAACAATTGTCTGGGACCATTTTGAATAAACTTTTTCTCAAACATTACGGGAC
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         Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 169546)

Hyman, R.W., Fung, E.L., Qin, F., Rowley, D., Mao, J., Tamaki, T.,

Kurdi, Q.B., Conway, A.B. and Davis, R.W.
Plasmodium falciparum 3D7 chromosome
                                                                Plasmodium falciparum
                                                                                                      AC004157.8 GI:9797712
                                                                                                                                 PROGRESS ***,
                                                                                                                                             AC004157 169546 bp DNA Plasmodium falciparum chromosome 12 clone
                                                                              Plasmodium falciparum.
                                                                                            HTG; HTGS_PHASE1
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Hyman, R.W., Qin, F., Fung, E.L., Conway, A.B. and Davis, R.W.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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Similarity 44.3%;
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/chromosome="12"
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23666: gap of unknown length
169546: contig of 145880 bp in length
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complement(1570.
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MEYCTLIKKGKYDNDMTYKLKEVIKATHHILCDKTKNLETFOSDIDYSTLLNSLNNK
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IFYKMENYKDFHFKLKDSDLLSIKLLSNTFVKINEVYNSYDFYLLFNNISCILYNFLV
RNSVKKYKDTYIYILNDLSFYYKYIKNNDRTKKKNFFLLSSSMKELICKNILSVSN
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KYEHRYIEYKKENLFINLNKIIBCLIKLNIFIYLKKKKTYLLYKGGLCPINLKENII
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TNKKIYKKSKAQSLFONGLNIHDKLILFKNLPXYKCAKXECISKEVYKYLLDDYKKC
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HEIYKLLFIFNKYLNNSNIPPNKNLIQEMEFNLYYFREIKNEKNYIIKMNKKEIYKK
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TVVTKRLNNYKTVSAPVKKFNNLNISLYRKNRTFALNTKRSKPVGTIKSSVPRKRIKK
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/db_xref="GI:3845199"
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/protein_id="AAC71887.1"
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/note="predicted by
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/codon_start=1
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Submitted (12-JUN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6: On Feb 5, 2002 this sequence version replaced gi:15625013.
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Submitted (05-FEB-2002) Genome
University School of Medicine,
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Direct Submission
Submitted (10-SEP-2001) Genome
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >-30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by This sequence was finished as follows unless otherwise noted:

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D McPherson, Department of Genetics, Washington University, St. MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc . Louis

SOURCE INFORMATION:

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Homo sapiens

donor, as described by Oscogawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998), An improved approach for construction of bacterial artificial chromosome libraries. Genomics Sill-B. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong VECTOR: DBAC-3 & The Construction of Date of the Property of the Computation of Pieter de Jong VECTOR: DBAC-3 & The Computation of Date of the Property of the Computation of Pieter de Jong VECTOR: DBAC-3 & The Property of The Computation of The Computat The RPCI-11 pBACe3.6 human BAC library was made from the blood of

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NEIGHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of RP11-724016;
Ar base position 172816 of RP11-724016.

Unresolved simple 25900. sequence repeat from base position

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2658. .2729
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19731. .20040
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19312. .19441
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SOURCE ORGANISM KEYWORDS

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VERSION 86827 bp DNA linear INV 04-MAY AL034556 AL008971 AL008972 AL008978 AL010141 AL010153 AL010162 AL01206 AL012010 AL139179 AL034556 AL01010141 AL010163 AL010164 HTG; centromero: Bowman,S., Lawson,D., Basham,D., Brown,D., Chillingworth,T., Churcher,C.M., Craig,A., Davies,R.M., Devlin,K., Feltwell,T. Gentles,S., Gwilliam,R., Hamlin,N., Harris,D., Holroyd,S., HTG; centromere; CTRP protein; initia Serine/threonine protein phosphatase. Plasmodium falciparum 3D7. Plasmodium falciparum 3D7. Eukaryota; Alveolata; 1 (bases 1 to 86827) Apicomplexa; Haemosporida; Plasmodium. initiation Feltwell, T.,

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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On or before May 14, 2001 this sequence version replaced g1:2982535, g1:2982536, g1:2894454, g1:2982554, g1:2982562, g1:2894489, g1:2982572, g1:2982574, g1:4493931. For more information about this sequence or the Malaria Project,
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Location/Qualifiers
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/gene="pFC0575w, MAL3P5.1"

/gene="pFC0575w, MAL3P5.1"

/gene="pFC0575w, MAL3P5.1"

/note="pFC0575w (MAL3P5.1), Hypothetical protein, len:
                                                                                                               /gene="PFC0575w, MAL3P5.1"
/note="predicted splice donor
PFC0575w (revised)"
                                                                                                                                                                                                                                                                                 816.
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FTMKLNIERNNKNII RSNYDMINNDISIDKOMYMNNDIDVNINNISIDEKIKEQFENP
DDENLKELKDTYEQFQLFNDNIIKYIEEDQPLYNINDNSHUMNINTMKRKHKK
DTYNDDDDYDYEKEEDLYJQKNIDDYIYKNTIGMNKSLEEFKNQFIEQADIIFQOHEIS
NVNLDQHGRVKSNDENTKSTEHIKNKNTINKGYDTELLQNQMENNFIKNIDNNISND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'translation-"MYLKNYYIYISSCFILFDLCFSFHLLKMKYKNHMNNMKSVTFFL
RSPQIYRKRFKRSIKNYSFKKKKKKLLHCFSKLDKIINNLSYIIKHEOMSNIT
NINNLTRIKOVTHKKKSMEFTKENKOILLHCVFSKLDFKIINNLSYIIKHEOMSNIT
VHSILNQISEKYKEKNDAENYLALHLFLLKDENITLFSMMHIMDFFKSKQKVIECIRD
                     complement(3354. .6644)
/gene="PFC0580c, MAL3P5.2"
complement(3354. .6644)
/gene="PFC0580c, MAL3P5.2"
                                                                                                                                                                                                                                                                                                                                                                                                I IMFNVM"
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/note="predicted splice acceptor
(revised of PFC0575w)"
                                                                                                                                                                                                                                                                                                                /gene="PFC0575w, MAL3P5.1"
/note="predicted splice do
PFC0575w /revised)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IKSKKKKKNLSIYINLFICTLIYFTYCMCLLIKYISHLCIFFFFFFCFFLCYNILER
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/strain="3D7"
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20575w, MAL3P5.1"
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  MAL3P5.2"
(MAL3P5.2),
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/protein_id="cab90285.1"
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TLKKEKKKIWNFSFSALSNDSNSYKKYIYDLTLDNIIESETKYNFASYGKVVV
TLKKEKKKIWNFSFSALSNDSNSYKKYIYDLTLLDNIIESETKYNFASYGKVVV
TLKKEKKKIWNFSFSALSNDSNSYKKYIYDLTLLDNIIESETKYNFASYGKVVV
TLKKEKKKIWNFSFSALSNDSNSYKKYIYDLTLLDNIIESETKYNDSV
QNFLKEEKNNSSKLQDDIDEDEEKYFDEEILREAKKSEEYDKDDEEL"
7790. . . 7799
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                     /note="potential
PFC0581w"
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/gene="PFC0581w"
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DQKKDILKKIYFLKGNKLDDIQILNELYVMIYMRLLFBCSLKLISIKKNIHLLEKKME
FDKDNKIIYLMSADYMNNLRRNILKRPSKNEBRENINSFASFPFLLSKNIIYFEDEIG
RSRDWTIYMNVDKETNKTTINNNNLNNDNICSNNDHICSNNDHICSNNDHICSN
NNNNICSNNNNNICSNNNNNICSNKMLDEFQDNKFNDYNTKKEKRK
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8302. .8368.8568. .8641,8713. .8812,8924. .9006,9122.
9369. .9505,9613. .9838)
/gene-"PFC0581w"
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hexExon"
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YKNKIKKYLTYLNNNISNDLYPYNISYNKIYNQNKYKNRKNFSHIFYSLKNDIHLLLF
LYTQRIQNCCDIFSYIYKKYNFNEKNPFLNYLYYELHYIVYSEKKKKKKFFSFISSSP
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KRREAIKYNFISDEQNLFNKFY IYEITUSYSKYKILSPHLSUTILKNISEHCYNIYP
SLYYYNKLDNKHNLLNEKKLKYFKOLINEHTOQAPTHHTHUNNNNKKEDLINHISC
KUTNISSYSTYNNWEKENINIYDKYNIHNFYTEKSISYKDENCOHITLUMIYLLNOTY
DNICRICLNTNTNIY INFYMLIKKYLKYKNEILLLAYNHIEDWKKKINQKNNTNTS
LFKYLYSFFFFKKEENHIYDLFEDAMNHLHKKENDKFYNYSNENTHUNIKYISON
FYDHINSSNRCSFKNLKKQOTDDNTKHIIMGKEKYPMNKSDHEKKNNNTCGNINIEK
tentative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="Hypothetical
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/db_xref="GI:4493932"
                  /note="PFC0581w, hypothetical protein, len: 324 aa, revised: new gene prediction, splicing prediction v
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                         prediction very
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Matches 1051;
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CCCGATATAGTTTTTGGTTCTGGATTAGGTTTATTTGATCATAATTACATGCATCATTTC
                                                                       GTTTTTGTGTTTTTGTTATATGTATATGAGTAAAATCAAAAAGAGTATTGAATTGAAGT 334
                                                                                                           ATCTTTACATTGTATTGTTATAACAAAATATCTATCTTTGGTATATGAGAAAATATGGAG
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PFC0581w"
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/note="potential splice acceptor sequence for exon
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Pred. No. 1.1e-09;
0; Mismatches 1307;
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                  ATCTTTTGGGTTACAGTTTCGAAGTCCTCTACAAGCGTGTAACCATCTGCAACTATTAAA
                                                                       AAACAAGAAAAAAAGAAAACGATTTTTCTTGGATTCCATTCAATGATCTAAAATGCATAG 1473
                                                                                                            ATTAATTTATAATAATATATATAGTATTTTTAATTATTTATTTTATGAAACATATTTATA
                                                                                                                                           AATATAATAATTATCATATTTATTTAT-TTTATTAAATTAAATTTAATATATAATTAAATT
                                                                                                                                                                                    TTAAGAGAAGTTAACATATCCATATATGGGTATGCTATACCTTTCACGTATGCTATACTA 1293
                                                                                                                                                                                                                                           GAAATCCTTTAGAAAATTTTGGAATTACCGGTTGTTATGTAAATATAGATTTTAGTGGTAA 1173
                                                                                                                                                                                                                                                                                GGGACACTGGACTCGACCCTTAAAATACGATTTTACAGCGTCACTAGTTGAGATTACTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATAATTAAATTTAATTATAAACATTTATTATATTTAATTAATTTAATTAAT--ATTTAT 40864
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Mammalia; Eutheria; Primates;
1 (bases 1 to 133877)
                                                                                                                                                                        AC120883
AC120883.2 GI:22123189
                                                                                                                                                                                                                               Homo sapiens chromosome 18 SEQUENCE, 4 ordered pieces
                                                                                            Homo sapiens
                                                                                                                                              HTGS_PHASE2; HTGS_DRAFT;
                                                                                                                                                                                                                                                               133877 bp
ne 18 clone
                                                                                                                                                                                                                                                               clone
                               Catarrhini; Hominidae; Homo
                                                            Craniata; Vertebrata; Euteleostomi;
                                                                                                                                              HTGS_FULLTOP
                                                                                                                                                                                                                                                         DNA linear HTG 06-AUG-200 CTD-2146H24 map 18, WORKING DRAFT
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Birren, B., Nubbaum.C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Conka, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Grand-plerre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacCanthy, M., Meldrim, J., Meneus, L., Mihova, T., Menga, V., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., O'liver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RS Biren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Chepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farroira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Godd, S., Goyette, M., Gashen, L., Grand-Pierre, N., Galders, S., Godd, S., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Muyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Norman, C., Retta, R., Rieback, M., Riley, R., Riese, C., Rogov, P., Ramond, C., Retta, R., Rieback, M., Riley, R., Riese, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Stauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trajillo, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zalnoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Aug 6, 2002 this sequence version replaced gi:20531967.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                 Center project name: L26769
Center clone name: 2146_H_24
Center clone name: 2146_H_24
Center clone name: Statistics
Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of read Assembly program: Phrap; version 0.960731
Consensus quality: 132654 bases at least Q40
Consensus quality: 132863 bases at least Q30
Consensus quality: 13265 bases at least Q20
Insert size: 133000; agarose-fp
Insert size: 133577; sum-of-contigs
Quality coverage: 17.1 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                     Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: WIBR
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BASE COUNT
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Local Similarity 44.1%;
                                                                                                          GAAGATTTTCTTACCAATTAAAATTTCGAATTCATATCTCTTGATTAAATTAAATTAC 526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGTGTGAATATCCGTTTATCGATCACTCCAATCATGATTATGATTCTTGTGCTAATCCA 586
                                                                                                                                                            TTGGTTCTGGATTAGGTTTATTTGATCATAATTACATGCA-TCATTTCTTTGATTACTAT 466
                                                                                                                                                                                                                                                                               ATAAAGGAAATAATCGATTCCATTTGGTTGGATTACACAGTTAAGTTTTTGTGTTTCTTT 290
                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the accession number will be preserved.

1 716: contig of 716 bp in length
717 816: gap of 100 bp
1588 1993: contig of 671 bp in length
1994 2093: gap of 100 bp
2094 133877: contig of 131784 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by the finished sequence as soon as it is available
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1588. .1993
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/db_xref="taxon:9606"
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                                                                                     CAGTTTCGAAGTCCTCTACAAGCGTGTAACCATCTGCAACTATTAAATTGCTTTTAA 1546
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                                                                                                                                                                                                                                                                     86827 bp
Plasmodium falciparum MAL3P5, cc
AL034556 AL008971 AL008972 AL008
AL010206 AL010210 AL139179
AL034556.3 GI:7711064
                                                                                                                                                     HTG; centromere; CTRP protein; initiation Serine/threonine protein phosphatase. Plasmodium falciparum 3D7. Plasmodium falciparum 3D7 Eukaryota; Alveolata; Apicomplexa; Haemosp 1 (Dases 1 to 86827)
                                                                                                                                                                                                                                                                                                                 P5, complete sequence.
AL008978 AL010141 AL010153
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99376085
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On or before May 14,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bowman, S., Skelton, J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lawson, D., Bowman, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ealciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 86827)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                more information about this sequence or the Malaria Project. http://www.sanger.ac.uk/Projects/P_falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complete nucleotide sequence of
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                                                     complement(3354..6644)
/gene="PPC0580c, MAL3P5.2"
complement(3354..6644)
/gene="PPC0580c, MAL3P5.2"
/note="PPC0580c (MAL3P5.2), Hypothetical protein,
1097 aa, possible signal sequence, predicted using
haxExon"
                                                                                                                                                                                                                                                                                                                                                                                                                                             RSPOIYKKFKKSKIKNVSFKKKOKKPLFLFENLKKGFSFLGFWRNQYDOKYIDDVIS

NINNLTRIKQVTHKKKSNEFTKENIKQILLHCVFSKIDFKIKNLSYIIKHFQWSNIT

VHSILNQISEKVWEKKDAENYLAHLFILKDENITIESSKIDFKIKNLSYIIKHFQWSNIT

VHSILNQISEKVWEKKDAENYLAHLFILKDENITIESSKIDFKIKNFSKYLEGING

IKSKKKKKNLSIYINLFICTLIYFTYCMCLLIKYISHLCIFFFFFFFFCFFLCYNILER

IYEECVODLIRKKIERYNLYCEKKKIKFHMKDAIKKMEINMKDDLYFWYHYDELLRC

FTMKLNIERNNKNIIRSNUDNINNDISIDKWHNNPIDVVINNISLDEK KROFFEN

DENLKELKDTYCOFQLENDNIIKYIEEDOPLYNINDNSNINNNNINTMKKHKIK

DOTYNDDDDYDYEKEEDDLYICKHIDDYYYKNTIGMKSLEEFKNOPIEOADIEFONFLS

NVNLDQHGRVKSNDENTKSTEHIKNKNTINKGYDTELLGXIEYLKFKYQYDIING

ISNNEINJIKLKKKLNQSDEDINLTSDLYYERLETKVLWYIQKIEYLKFKYQYDIING

TSNNEINJIKLKKKLNQSDEDINLTSDLYYERLETKYLWYIQKIEYLKRYQYDING

YPIIKNEKTYLLDLLNYGYKIVMSPDVDNSLFEKTKIDSIPNEKDKNNQMENQKNSKNY
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complement()?"
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/gene="PFC0575w,
/note="predicted
                                                                                                                                                                                                                                                                         /gene="PFC0575w, MAL3P5.1"
/note="predicted splice acceptor
(revised of PFC0575w)"
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/gene="PFC0575w, MAL3P5.1"
/oin(322. .603,826. 1023,1197. .1301,1458.
/product="Hypothetical
/protein_id="CAB38968.1
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/note="predicted
                                       /codon_start=1
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/db_xref="GI:7711065"
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/note="PFC0575w (MAL3P5.1), Hypothetical protein, len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation-"MYLKNVYIYISSCFILFDLCFSFHLLKMKYKNHMNNMKSVTFFL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="SPTREMBL:097258"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MKKKKHYFSIKFYNVDKNKYYLCSKDYIRIINYMIGLHIFRLL
QKIPHIYFANEQIASSFFESHKNYRYTKEDIIDGIEKCWFNITDYLISESIKQDNDFS
NDIKTTYTAMKNKMOLLTTSYSNKKIDTVNASFQWAQSPEYIFLNIKFSHRWSSPGA
LKYKDEEIVSKKNNFSFSALSNDSNSYTKKYIYDLTLLDNIIESETKYNFASYGKYYY
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FYDHINSSSNRCSFKNLKKQQTDDNTKHIIMGXEKYDMKSDHEKKNNNTGGNINIEK
DQKKDLIKKI YELKGNKLDDIQILMELLYMNYMRLLFESCELKLIS IKKNIHLLEKKME
FDKDNKIIYLNSADYMNNLRRNILKRFSKNEERNINSFASFPFLLSKNIITYFEDEIG
RSRDNTIINNVDDKETWKTTHNNNDNDNICSNNDHICSNNUDHICSNNUDHICSN
NNNICSNNUNICSNNUNICSNNUNNINIGSNWALDEFCDNKFNDYNTRKKEKRKI
YELAKTYTNNIFDYLKGKKEKHQNEDNTINLYYIKKKFPHIFYLKNIIKNDTSFIEH
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                                                                                    /gene="PFC0581w"
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                                                                                                                                                                                                                                                 PFC0581w
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                                                                                                                                                                                                                /gene="PFC0581w"
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/protein_id="CAB90285.1"
/db_xref="GI:7711066"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="PFC0581w"
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KIKKIRIHNKOSYIPILFLNIYDSYIYKNKILRWLYFKFRKRKDKEEYYYITNNVFK
KRREAIKYNFISDEQNLFNKFYIYEIVLEYSLKYGILSPHLSLYILKNISEHCVNIYP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNICRICLNTNIYINEYMINILKYICYKNMEIILLNYNHIEDMKKKINQKNNTNTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="GI:4493932"
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                            41000 TAACTATATATATATATATAAATAAAAATTAATTATTATATAATTAGATTTAATTATAT
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                                                                                                                                                        TAAATATACATATAAATTAAATTAAATATAATATAAT
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                                                                                                                                                                                                                                                                                                                                                   ATAATAAAGGAAATAATCGATTCCATTTGGTTGGATTACACAGTTAAGTTTTTGTGTTTC 287
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/note="potential splice acceptor
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TCCATTAATATTTTTTGAAATCTACAAATTATTAATATTTAGTCAATAACAATGCATAGA 2143
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2 (bases 1 to 205130)
Waterston,R.H.
Direct Submission
Submitted (04-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
                                                                                                                                                                                                                           AC105425
AC105425.2 GI:18151067
AC105425.2 GI:18151067
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Homo sapiens chromosome 7 clone RP11-776N17, WORKING
SEQUENCE, 12 unordered pieces.
                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Primates;
1 (bases 1 to 205130)
Waterston, R.H.
                                                                                                                     The sequence of Homo sapiens clone
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                                                                                                     Jnpublished
                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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COMMENT
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Insert size: 203204; sum-of-contigs
Quality coverage: 10.60 in 020 bases; agarose-fp
Quality coverage: 10.87 in 020 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site:http://genome.wustl.edu/gsc/index.shtml
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/db_xref="taxon:9606"
/chromosome="7"
                               vector_side:left"
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1257. .2523
                                                                   /note="assembly_name:Contig110
                                                                                                                                            note="assembly_name:Contig108"
                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                        note="assembly_name:Contig109"
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                GATCACTCCAATCATGATTATGATTCTTGTGCTAATCCAGCAAATTATTAACAAGAGTAT 607
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204024. .205130
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                                                                                                                                                                                                                                                 Submitted (28-JUN-1994) Laurie S. Kaguni Ph.D, Dept. of Biochemistry, Michigan State University, East Lansing,
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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            /rpt_type=tandem
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/note="repeat I-C/A"
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/organelle="mitochondrion"
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Mitochondrion Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 12511 to 12682)
    Drosophila
                                                                                                               Clary, D.O., Wahleithner, J.A. and Wolstenholme, D.R. Transfer RNA genes in Drosophila mitochondrial DNA:
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Lewis, D.L., Farr, C.L., Farquhar, A.L. and is Sequence, organization, and evolution of 1 Drosophila melanogaster mitochondrial DNA Mol. Biol. Evol. 11 (3), 523-538 (1994)
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88174373
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Drosophila melanogaster mitochondrial DNA: complucientide sequence and evolutionary comparisons Insect Mol. Biol. 4 (4), 263-278 (1995)
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                                                                                                                                                                                                                                                                                                          Submitted (03-OCT-1995) Laurie
                                                                                                                                                                                                                                                                                                                            Lewis, D.L., Farr, ODirect Submission
                                                                                                                                                                                                                                                                                                                                                                                     Insect Mol. 96423163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified arthropods
Science 258 (5086),
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Ballard, J.W., Olsen, G.J.,
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Nature 304 (5923), 234-241 (1983)
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/product="tRNA-Gln"
171. .239
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           /product="NADH dehydrogenase
/protein_id="AAC47811.1"
/db_xref="GI:1166530"
                                                                                                                                                                                /note="derived from new and previously submitted sequences; sequence is a composite containing seobtained from different Drosophila melanogaster
                                                                                                                                                                                                     sequences;
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                                                                                                                                                                                                                                          /organism="Drosophila melanogaster"
/organelle="mitochondrion"
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                                                                                                                                                                                                                            /db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                           Farr, C.L. and Kaguni, L.S.
                                                                                      .1265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Faith, D.P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (1992)
                                                                                                                                                                                                                                                                                                 S. Kaguni,
t Lansing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (24), 9558-9562 (1990)
                                          subunit
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                                                                                                                                                                                                                                                                                                 , Biochemistry
MI 48824-1319,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kaguni, L.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                               completion
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trna tRNA tRNA

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LKSGAAPFHFRFRIMMEGLTMINIATMOK 1APLILSTYLIKYLLLLISVIESVIE
GAIGGLIQTSLKKLMAPSSINILGMMLSSLM ISESIMLLIFFFYSFLSFVLTFEKENIF
KLFHLINQLESWFVNSKIIKFTLEMNFLSLGGLPPFLGFLPKWLVIQQLTLCNQYFWLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="tRNA-Lys" 3840. .3906
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3768. .3838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="tRNA-Leu" 3083. .3767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAILMALGFVFLFTVGGLTGVVLANSSVDIILHDTYYYVAHFHYVLSMGAVFAIMAGF
IHMYPLFTGLTLNNKWLKSHFIIMFIGVNLTFFPQHFLGLAGMPRRYSDYPDAYTTWN
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                                                                                                                                                                                       /translation="MMTNLFSVFDPLAIFNFSLNWLSTFLGLLMIPSIYWLMPSRYNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="tRNA-Asp"
3907. .4068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="TAA stop codon residues to the mRNA"
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join(1470. .1472,1474. .3009)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMMSTLITLFFYLRICYSAFMMNYFENNWIMKMNMNSINYNMYMIMTFFSIFGLFLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_except=(pos:3767,aa:TERM)
/transl_table=5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IVSTIGSTISLLGILFFFFIIWESLVSQRQVIYPIQLNSSIEWYQNTPPAEHSYSELP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAIGLLGFIVWAHHMFTVGMDVDTRAYFTSATMIIAVPTGIKIFSWLATLHGTQLSYS
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/transl_table=5
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                                                                                                                                                                LTANMIAGHLLLTLLGNTGSSMSYMLMTFLLMAQIALLVLESAVAMIQSYVFAVLSTL
                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLNSMNWKW"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="ATPase 8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=5
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/db_xref="GI:1166532"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="cytochrome c oxidase subunit
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                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=]
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      oxidase subunit
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 TCATTTAAAATATTTACAAGTAATTAATTATCTTTACATTGTATTGTTATAACAAAATAT 185
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                                                                                               TTTTTAAAAAATAAACAAAAATTTTTAATAAATAATTTTTATAATGAAATATAATTTAT 17656
                                                                                                                                                                                                                                                                                                                                                                                                                TTTTAAAAATTTCTTAAATGTATTATTTTTATAAAAAATATTTATATAATAAAAATCATGT
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                                                                                                                                                          ATTGAGAAAAACCGAAAATAAGAAAAGGGAAAGAGTAGTGACCCATGGAGTATGTGAAT 665
                                                                                                                                                                                                                        TCGATCACTCCAATCATGATTATGATTCTTGTGCTAATCCAGCAAATTATTAACAAGAGT 605
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VLGNIITILTYYQWWRDVSREGTYQGLHTYAVTIGLRWGMILFILSEVLFFVSFFWAF
FHSSLSPAIELGASWPPMGIISFNPFQIPLLNTAILLASGVTVTWAHHSLMENNHSQT
TQGLFFTVLLGIYFTILQAYEYIEAPFTIADSIYGSTFFMATGFHGIHVLIGTTFLLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="tRNA-Asn" 6184. .6251
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6055. .6118
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/protein_id="AAC47817.1"
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/db_xref="GI:1166535"
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                                      TATTTTCGCGATGCATGAAGGATAAACCTAATGACTTTAATTTTTTGAAAATGTAACCCT
                                                                           TTAATCTTGTTTCCTACGGTATAAATATTAATCATCGAGGTAAAAAAAGTTTTGTCT
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ATGCATGGTGCGATTCAGAATTGGGACAACAATGAAAACGGAATTAAAATATTAACTTTA
                                                                        TAATATAATGATTTAATTAATTATTATATATTATAAATTTATATATATTATTGAATATTTA
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                                                 TAACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTT
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Search completed: March 30, 2003, 08:19:09 Job time: 34395.6 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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DB seq length: 2000000000
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11274.505 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DWF4; cytochrome P450 enzyme; brassinosteroid; 22alpha-hydroxylation; plant phenotype; cell elongation; ss.
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Sequence encoding	Cally D	•				cho-ie-Nyst	eummi	T CIGUSO	signal suppressor	DWA CERTIPTION	CHEMICALLY pretrea	chair immune syste	genome		Immune	Immune	genome	Immune	immune	odium va	Plasmodium var-7 g	nlagarianne syste		genon		Chemically treated	cDNA encoding a SC	Human breast cance	\vdash	Buchnera sp. genom		Human immune syste	ra	Tumour suppressor	

ALIGNMENTS

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells.
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Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
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407; Conserv
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                                                The invention relates to a nucleic acid, which comprises a segment of the chemically pretreated DNA of genes associated with DNA transcription from one of 346 sequences, and an oligomer, in particular an oligonucleotide or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical to the chemically pretreated DNA of genes associated with DNA cranscription. The set of oligomer probes are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleic acids are useful for diagnosing or treating diseases associated with DNA transcription (particularly with the methylation status), e.g. adenosine deaminase deficiency, viral infection, retroviral infection, Sezary syndrome, tuberculosis, developmental disorders, sporiasis, Rieger's syndrome, cubroculosis, developmental disorders, sporiasis, Rieger's syndrome, neurological disorders, neurodegenerative disorders, Warner syndrome, syndrome, Niemann-Pick disease, myelodysplastic syndrome, myocardial confarction, hypertension, anglogenesis, erythropoiesis, congenital heart disease, HDR syndrome, arthritis, polyglutamine disorders, solid tumours or cancer. Sequences DARXB8127-ABRXB472 represent DNA transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-APR-2000;
07-APR-2000;
30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, sol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABK28257;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Olek
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TATAGTTTTAGTGGTATTTTTTTTTTAAATTATAGTGTAATATTTAAGTGTTTTTAAAAT
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                  TAGGAATTCAATGCTACTATCAATAGAAGAAACAGCTGAGTATTACATTTTAATTTAAAG 1936
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diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with cytosine methylation .
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                                                                                                                                                                                                                    CATCGAGGTAAAAAAGTTTTGTCTTATTTTCGCGATGCATGAAGGATAAACCTAATGAC 176:
                                                                                                                                                                                                                                                                                                                           AAATACATACTTTGGATGTTTAAACTTAATCTTGTTTCTTCCTACGGTATAAATATTAAT 170:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATAAGAGCGAACTTGTAACATTACAATATTTATATTAGATACTAGTATGTGATTATTCC 1641
GTTGCCATAATGACAGCCTCTACAACTGTGATAGTCAATTTTTTCTGCAAATAT-TAAAT 1876
                                                       TTTAATTTTTGAAAATGTAACCCTTTTACTCATAGATTA----ATTACCGTATGTTTTT
                                                                                                                                                               TAGATTTATTAAAGATTTTTTTATTGTTTGTAAAATAATTTGTAAGTTTTTGATTTGGAAT
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                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; immune system disease; cytosine methylation; antiasthmatic;
antiarteriosclerotic; antianaemic; cytostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immune system associated gene SEQ ID NO: 399
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2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arterioscierosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, ALDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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AATGCATGGTGCGATTCAGAATTGGGACAACAATGAAAACGGAATTAAAATATTAACTTT
                                                  ATRACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAATATATACATTAAGCAAATT
                                                                                                                                ATATAATATATGTTTATATATATATATATGTAAATATATATATATATGTAAATATATATGTA
                                                                                                                                                        ATTAATATTTTTTGAAATCTACAAATTATTAATATTTAGTCAATAACAATGCATAGAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention provides a number of human immune system associated are modified by the methylation of cytosines. The sequences
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Pred. No. 0.
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06-APR-2000;
07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                                                       Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CpG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, graft-versus-host disease,
                1400
                                                                                                                                                                                                                                                                                                                                                                                 Designing primers and probes for analysing diseases associated with cytosine methylation state e.g. arthritis, cancer, aging, arteriosclerosis comprising fragments of chemically modified genes associated with cell cycle -
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                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                      Claim 1;
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arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic;
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 AACAATAAAAACAAAAACAAGAAAAAAGAAAACGATTTTTCTTGGATTCCATTCAATGA 1459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cycle; human; CpG dinucleotide; cytosine methylation; HIV; aging;
immunodeficiency virus; neurodegenerative disorder; solid tumour;
                                                                                                                                            glomerular disease, Lewy body disease,
Similarity
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                                                                                                                                                                                                                                                                                                                                                    SEQ ID No 93; 28pp;
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2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
                                             Conservative
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                                                                                                   B₽;
                                                                                                                                solid tumours
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                                          Score 82.6; DB 2:
Pred. No. 0.00032
0; Mismatches 57
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                       TTCTGACTATTGA 2428
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23-APR-2002

(first entry)

ABK28233 standard;

DNA;

15732

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CC Chemically pretreated DNA of genes associated with DNA transcription from CC one of 346 Sequences, and an oligomer, in particular an oligonucleotide or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical transcription. The set of oligomer probes are useful for detecting the CC transcription. The set of oligomer probes are useful for detecting the CC in a chemically pretreated DNA of genes associated with DNA cytosine methylation state and/or single nucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleic acids are useful for defection, retroviral infection, sezary syndrome, CC diagnosing or treating diseases associated with DNA transcription CC disconsing of the methylation status), e.g. adenosine deaminase CC haematological disorders, immunological disorders, werner syndrome, cc tuberculosis, developmental disorders, psoriasis, Rieger's syndrome, tuberculosis, developmental disorders, psoriasis, Rieger's syndrome, CC syndrome, Netwann-Pick disease, myelodysplastic syndrome, myocardial cf. disease, HDR syndrome, arthritis, polyglutamine disorders, solid tumours or cancer. Sequences ABX28127-ABX28147 represent DNA transcription consociated genomic DNA molecules of the invention.

CC specification but was obtained in electronic format directly from the curonean Patent office.
         Matches 453;
                          Query Match
Best Local
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30-JUN-2000;
01-SEP-2000;
                                                                             Sequence 15732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID No 107; 32pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, solid
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Score 82.6; DB 2.
Pred. No. 0.00032
0; Mismatches 57.
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                                                                      2672 G;
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                                      ATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGCCTATACGCGCTC
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                                                                                                                                ATTTTTCAAACATAATTAACAAACTTACTTAAAAAAACTTTATCTTACTTAAATAAAATTT
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ID AAS45384 standard;
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Best Local Similarity
Matches 285; Conserv
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06-APR-2000;
07-APR-2000;
30-JUN-2000;
 2050
                                                                                                                                                                                                                DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, graft-versus-host disease, aging, glomerular disease, Lewy body disease, arthritis,
                          1884 TCAATGCTACTATCAATAGAAGAAACAGCTGAGTATTACATTTTAAATTTAAAGACAAAAT
                                                                                                                                                                                                                                                                                                                                       Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CPG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Designing primers and probes for analysing diseases associated with cytosine methylation state e.g. arthritis, cancer, aging, arteriosclerosis comprising fragments of chemically modified genes
                                                                                                                                                                            Sequence 5689
                                                                                                                                                                                                                                                                                                                                                                                                                                                             associated with cell cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human immunodeficiency virus; neurodegenerative disorder; solid tumour; graft-versus-host disease; glomerular disease; Lewy body disease; cancer; arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-602751/68.
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                                                                              ATAATGACAGCCTCTACAACTGTGATAGTCAATTTTTTCTGCAAATATTAAATTAGGAAT 1883
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; 2000DE-1019058.
; 2000DE-1019173.
; 2000DE-1032529.
; 2000DE-1043826.
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                                                                                                                   Conservative
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                                                                                                                               Score 81.6;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                   Mismatches
                                                                                                                                                                                                          and cancers.
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genes and analysing

of chemically modified genes associated with tumour suppressor oncogenes, useful in designing primers and probes for diseases associated with cytosine methylation state e.g.

2001-602752/68

cancer

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ID AAS46426 standard; DNA; 5689
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06-APR-2000;
07-APR-2000;
30-JUN-2000;
01-SEP-2000;
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                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                           cytosine methylation;
                                                                                                                                                                                                                                                    cancer;
                                                                                                                                                                                                                                                           Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATAAAAAAATATTTAATAACGTTAAAAATATAAATATAT 1531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTATGTTCTTAAAATATTTTTTTTTTATATTTAGTTATAAATACATTATGAACCAATAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     suppressor
                                                                                                                                                                                                                                                   tumour; CpG
                                                                                          EPIGENOMICS
                                                                      Piepenbrock
                                                                                                          2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
                                                                                                                                       2000DE-1013847
2000DE-1019058
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                                                                                                                                                                                                                                                                                                (first entry)
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27pp; English.

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CC The invention relates to a nucleic acid comprising a sequence of 18 CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with CC bisulphite, of genes associated with tumour suppression and CC oncogenes having a sequence taken from 536 (actually 533 since CC (SS) and sequences complementary to (cs). The nucleic acid may be a CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may CC form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an CC array for analysing diseases associated with CpG dinucleotides e.g. CC ascertaining genetic and/or epigenetic parameters for the diagnosis cand/or therapy of existing diseases or the predisposition to specific CC and/or therapy of existing diseases or the predisposition to specific CC diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the cc differences serving as basis for diagnosis and/or prognosis events which CC 33 genomic sequences derived from tumour suppressor genes and CC complementary sequence of the corresponding odd numbered sequence (e.g. CC D2 and IDI, ID 536 and ID 535, except for those whose partner sequence CC is missing).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not of the printed specification, but was obtained i format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
AAAACGGAATTAAAATATTAACTTTAAAATAAATAAAAAT
                                                                        TGTTATCTAGTAGGTGTAATTAATA-ATGCATGGTGCGATTCAGAATTGGGACAACAATG
                                                                                                                    GTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGCCTATACGCGCTCAAAGTA
                                                                                                                                                                                           TTTTTTTTTTTTATGGAACAAGAAATAACAGATAGAAAACTATTTTGTTGTGGAATGGAA
                                                                                                                                                                                                                                                                                                     TAGTCAATAACAATGCAT-AGAAAGTTCCAAAAAAATTTTGTTAACAGAAACTTCCAAA
                                                                                                                                                                                                                                                                                                                                       AATAAATATTAAATTAAATTATTTTTTATATATATAAAATAAATAAATAATTANTAAAAAT
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Pred. No. 0.00044;
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1570 ATAAAAAAATATTTAATAACGTTAAAAATATAAATATAT 1531
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DNA transcription associated complementary genomic
                                                                                                 ABK28226;
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                                                                                                    standard; DNA; 5689
                                                                                             (first entry)
                                                                                          DNA #50
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viral infection; Sezary syndrome; haematological disorder; tuberculosis; immunological disorder; Werner syndrome; developmental disorder; psoriasis; Rieger's syndrome; neurological disorder; erythropoiesis; neurodegenerative disorder; Waardenburg syndrome; Niemann-Pick disease; myelodysplastic syndrome; myocardial infarction; hypertension; arthritis; angiogenesis; congenital heart disease; HDR syndrome; gene therapy; polyglutamine disorder; solid tumour. DNA transcription associated gene; peptide nucleic acid, PNA-ol PNA; cytosine methylation state; SNP; retroviral infection; gen single nucleotide polymorphism; adenosine deaminase deficiency; PNA-oligomer; gene; ds;

Unidentified.

WO200192565-A2

06-DEC-2001.

06-APR-2001; 2001WO-EP03973

06-APR-2000; 07-APR-2000; 30-JUN-2000; 01-SEP-2000; ; 2000DE-1019058. ; 2000DE-1019173. ; 2000DE-1032529. ; 2000DE-1043826.

(EPIG-) EPIGENOMICS AG

Olek A, Piepenbrock C,

WPI; 2002-090046/12

New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, solutionurs or cancer

Claim 1; SEQ ID No 100; 32pp; English

CC The invention relates to a nucleic acid, which comprises a segment of the CC chemically pretreated DNA of genes associated with DNA transcription from CC one of 346 sequences, and an oligomer, in particular an oligonucleotide CC to the Chemically pretreated DNA of genes associated with DNA transcription. The set of oligomer that hybridises to or is identical CC transcription. The set of oligomer probes are useful for detecting the CC in a chemically pretreated genomic DNA. The nucleic acids are useful for C in a chemically pretreated genomic DNA. The nucleic acids are useful for CC in a chemically pretreated genomic DNA. The nucleic acids are useful for CC in a chemically pretreated genomic DNA. The nucleic acids are useful for CC in a chemically pretreated genomic DNA. The nucleic acids are useful for CC diagnosing or treating diseases associated with DNA transcription CC disease, with the methylation status), e.g. adenosine deaminase CC deficiency, with the methylation status), e.g. adenosine deaminase CC deficiency, viral infection, retroviral infection, Sezary syndrome, CC deficiency, viral disorders, immunological disorders, werner syndrome, CC uncological disorders, neurodegenerative disorders, werner syndrome, CC syndrome, Niemann-Pick disease, myelodysplastic syndrome, myocardial CC disease, HDR syndrome, arthritis, polyglutamine disorders, solid tumours CC associated genomic DNA molecules of the invention.

Note: The sequence data for this patent did not form part of the printed CC European parent office. European Patent Office

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ARESULT 12
ABL33054
ID ABL333054
AC ABL33
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DT 26-MA
DT 26-MA
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                                                      03-JAN-2002.
                                                                                                                                                                                                                                        acute myeloid leukaemia; Alzheimer's disease; AIDS; neurofibromatosis; rheumatoid arthritis; psoriasis;
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antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
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                   genes which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
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                                                                                                          Claim
                                                                                                                                                                                                                                                                                          02-JUL-2001; 2001WO-EP07537
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                                                                                                                                                                                                                                                                                                                                          WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                          gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; immune system disease; cytosine methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL32891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL32891 standard;
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                                                                                                                                                                                                      Piepenbrock
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                                                                            invention provides a number of human immune system associated
                                                                                                         ID NO 864;
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2000DE-1043826
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                                                                                                         German.
                                                                                                                                                                                                                                                                                                                                                                                                      bowel disease;
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abnormal
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TTTAGAAATGTTAGAA
                                                      AACGGAATTAAAATATTAACTTTAAAATAAAATAAAAATTTGAGTAAATGTGTTTTCTGAC
                                                                        GTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAATTGGGACAACAATGAA
                                                                                                             TTTTTGGATTTTTAAGAGGATATTTATTAGTTAATTTTGTTTATAA-CGTTTAGTTTTT
                                                                                                                                                 ATTTTATGATAATTATAAGGGAAATGATTATTTTAGATTATAGTTTTTAGAAATGTTTA
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437; Conserv
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a gene (I) derived from Buchnera sp. CC containing the DNA (a) or (b), (a) has a fully defined base pair CC sequence selected from a table of sequences found in the Buchnera sp. CC genomic DNA of ABA92787 given in the specification or is a DNA selected from complementary DNA sequences, and (b) is a DNA which hybridises with the DNA (a) and encodes a protein. Also described are: (1) a recombinant vector (II) containing (I); (2) a transformant (III) containing (II); (3) a genomic DNA of Buchnera sp. containing the sequence given in ABA92788; (4) a plasmid derived from the sequence given in ABA92788; (d) a plasmid derived from the sequence given in ABA92788 and (d) is a plasmid which hybridises with a DNA; and (5) a method for the preparation of a protein in which (III) is cultured and the expression protein of the objective protein is collected from the resultant culture. The DNA is useful for developing agricultural chemicals for exterminating cockroaches. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-126043/17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABA92787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABA92787 standard; DNA; 640681 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specifically claimed Buchnera sp. genomic DNA sequence, from the
                                                                                                                                                                                                                                                                                                ATATTGTTAGTATTCTTTTTTATATTACCAATATATTTATCATCAATTAATATTGGCAAC 324745
                                                                                                                                                TCTTCTATCATGTAAAAATAATCAATTTCTTTAATATCAATAATTCTTTTAATATAT
                                                                                                                                                                                                                       AAATCTTTTGTACAAAGAAATAAAATATTATTTTTTTTATCTATAAATCCATTTTTGATC 324805
                                                                                                                                                                                                                                                            AGATACTAGTATGTGATTATTCCAAATACATACTTTGGATGTTTAAACTTAATCTTGTTT 1678
                                    TTAATTACCGTATGTTTTTGTTGCCATAATGACAGCCTCTACAACTGTGATAGTCAATTT 1858
                                                                         GCATGAAGGATAAACCTAATGACTTTAATTTTTTGAAAATGTAACCCTTTTACTCATAGA 1798
                                                                                                                                                                                  CTTCCTACGGTATAAATATTAATCATCGAGGTAAAAAAAGTTTTGTCTTATTTTCGCGAT 1738
                                                                                                                                                                                                                                                                                                                                                                           al Similarity
395; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                               640681 BP; 237522 A; 83822 C; 84757 G; 234580 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cockroach-symbiotic bacterium; cockroach
                                                                                                                                                                                                                                                                                                                                                                           Conservative
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45.8%;
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Pred. No. 0.00086;
0; M1smatches 455;
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WPI; 2002-147896/19
                       Olek A,
                                                                         30-JUN-2000;
01-SEP-2000;
                                                                                                                                        03-JAN-2002
                                                                                                                                                                                                                              Human; signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cance antitumour; cytostatic; mutant; ds.
                                                                                                              29-JUN-2001; 2001WO-EP07472
                                                                                                                                                                W0200200926-A2
                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                               Signal transduction associated gene modified complementary DNA #177.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 their complementary sequences.
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to chemically modified DNA sequences of signal transduction associated genes who have a contract the sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction -
TTTATATTAGATACTAGTATGTGATTATTCCAAAT----ACATACTTTGGATGTTTAAA 1665
                                                                   ATATACTTATCTACCTTTTAAAACAAAATACACTAAATTTAATTTAATCTCTTAAATAAC
                                                                                                  TCTTTAACATATTTATTGTTAGTTGGAATTTAATAAGAGCGAACTTGTAACATTACAATA 1610
                                                                                                                                                                    TTCGAAGTCCTCTACAAGCGTGTAACCATCTGCAACTATTAAATTGCTTTTTTAATGCA 1550
                                                                                                                                                                                                                                    AACGATTTTTCTTGGATTCCATTCAATGATCTTAAAATGCATAGATCTTTTGGGTTACAGT 1490
                                                                                                                                     AAATTATTTTAÄAATTAAACACATACACACTAATCTAAAATAACTATAATCCATATAAC-
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Pred. No. 0.00094;
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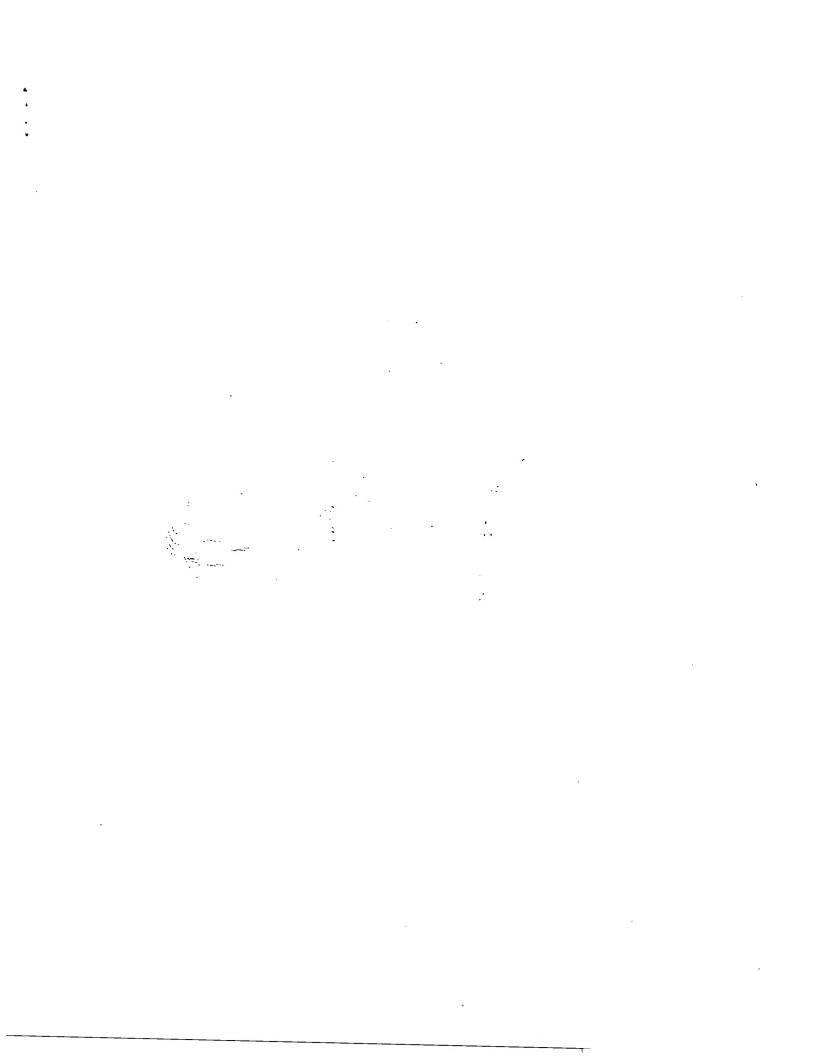
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                                               TTTTATATTTAGTTATAAATACATTATGAACCAATAATAGTTGGTGAATTCAAATATCTC
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Search completed: March 29, Job time : 2214.58 secs 2003, 18:59:11



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Result
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Maximum DB
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Listing first 45 summaries
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Perfect score:
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seq length: 2000000000
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/B_COMB.seq:*
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US-08-947-823-1
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US-08-947-838-124
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              Sequence 13, Appl Sequence 186, App Sequence 137, Appl Sequence 137, Appl Sequence 1517, Appl Sequence 1517, Appl Sequence 1517, Appl Sequence 1517, Appl Sequence 27, Appl Sequence 288, Appl Sequence 288, Appl Sequence 1, Appl Sequence 36, Appl Sequence 37, Appl S
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                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-193
ATTORNEY/AGENT INFORMATION:
NAME: ISTACLSON, Ned
REGISTRATION NUMBER: 09,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEPHONE: (619) 235-8550
TELEPHONE: (619) 235-8550
TELEPAX: (619) 235-8550
INFORMATION TOR SEO ID NO: 13:
SEQUENCE CHARACTERISTICS:
FRACTH: 19124 base pairs
                                                                ; ANTI-SENSE: US-08-487-826B-13
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      Query Match
Best Local Similarity
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Patent No. 5993827
GENERAL INFORMATION:
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                                                                      LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
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APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOWAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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CITY: Newport Beach
STATE: California
COUNTRY: US
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O Newport Center Drive 16th Floor
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US-09-426-290-1
US-08-749-391-1
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US-07-638-431-1
PCT-US92-00018-1
US-09-316-083-2
US-08-913-842-3
US-08-913-842-6
US-07-98-11-8678-8
US-08-107-755A-8
US-08-107-755A-8
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US-08-617-8608-32
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Score 77.4; DB 2;
Pred. No. 1.8e-06;
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              Length 19124;
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                                    TTTAGTTATAAATACATTATGAACCAATAATAGTTGGTGAATTCAAATATCTCCATTAAT 2092
                                                                        TGAGTATTACATTTTAAATTTAAAGACAAAATTTTTTGAAAAATGTTATAATTTCTAACAAT 1972
                                                                                                                                                                                                                                                        CAATTTTTTCTGCAAATATTAAATTAGGAATTCAATGCTACTATCAATAGAAGAAACAGC
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                                                                                                          TTATTTTCAAATACAATTAATTAGATTTCTTAAATATTTCTTCATTTATTCATTTTATA 882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                       REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                               APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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APPLICANT: Rebettle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
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                                    TYPE:
               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                  nucleic acid
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Steiner, Sabine
Mohr, Christine
                                                                                                          919-541-8689
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MOLECULE TYPE: ORIGINAL SOURCE:

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US-08-487-826B-13/c
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                                                                                                                                                                                                                                                                                          Sequence 13,
Patent No. 5
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Best Local Similarity
                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                             APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE
NUMBER OF SEQUENCES: 45
                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                            92660
                                                                                                1: 620 Newport Center Drive
Newport Beach
California
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5993827
                                                                                                                                                                                                                                     Sim, Kim L.
Chitnis, Chetan
Miller, Louis H.
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Pred. No. 4.6e-05;
0; Mismatches 279;
         Version #1,25
                                                                                                                        16th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (619) 235-01 INFORMATION FOR SEQ ID NO:
                                      1077
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HYPOTHETICAL: N
ANTI-SENSE: NO
6387 TATTTTTTATGTATTTCATGCATTTTATGAATTTCAAAATTTTATTGTATAATATAAAA
                                                                 6444
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LENGTH: 19124 base pai
                                                                                                                                                                                                                                                                                                                                                                                       717
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   420 TAGGTTTATTTGATCATAATTACATGCATCATTTCTTTGATTACTATGAAGATTTTCTTA 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Israelsen, Ned REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
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                           AAGCTATTTATACAAAGTTACAAACTGAATATAGCTTGAAATCCTTTAGAAAATTTTGGA 1136
                                                                                  AATACGATTTTACAGCGTCACTAGTTGAGATTACTAGCATAAAGCATAAAGGACCCGTTC 1076
                                                                                                                                                                       ATTATTATATTATATTATTATTATTAATAAAAAATGTTTTTATCATT---TGTTTTGTTG
                                                                                                               TGGGACCATTTTGAATAAACTTTTTCTCAAACATTACGGGACACTGGACTCGACCCTTAA 1016
                                                                                                                                                                                                                                ATCATATTTATATATTCATATATATATAATTGATATAGATACATATTCTTTGTATTGTTG 6565
                                                                                                                                                                                                                                                                                                              AAAATTTGCGATAACGATTGTGAAAAATATTTTATTTGTTAGCTGATCTCAATATTATGT 836
                                                                                                                                                                                                                                                                                                                                                                           CCCTGCCAGCTTTCTCTCACAATCAATATCGACCCTATTTGGATTTTCTGGATATTCGTT 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCTTAACTATATTATCGCGGATATATGATAACAATGATATATCACAAAACAATTGTC 956
                                                                                                                                                                                                                                                          AAAAATACGAAAATACAAACATATAAAAAAGTATATATGCAACGTGTTTATATATTTAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGAGTATTGAGAAAAAACCGAA----AATAAGAAAAGGGAAAGAGTAGTGACCCATGGAG
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519) 235-0176
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Pred. No. 0.00016;
0; Mismatches 1091;
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2208 AACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTT 2267
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                                                          GACTTATTATTCAGTATTCTTATTTATTTTTTTTTTTTCCTTATTAAGATTAAAATAA
                                                                                                                                                                                                                                   ---ATATTTTTTGAAATCTACAAATTATTAATATTTAGTCAATAACAATGCATAGAAAGT 2147
                                                                                                                                                                                                                                                                                                                                                        TTAGTTATAAATACATTATGAACCAATAATAGTTGGTGAATTCAAATATCTCCATTA---
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                                                                                                                    TTTCTATAATACATGTTACGTATTTGTAATTATGTTACATTTTTAAAAAATGTATAATAT 5382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---TATTTAAATATTTTTCAAAAAACTAATCATGTTAATATAATATAATATAACATAAAT
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                                                                                                                                                                                                                                                         TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 615 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6239264 GENERAL INFORMATION:
                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 186, Application US/08998416
                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 001
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                    APPLICANT:
APPLICANT:
APPLICANT:
 1810
                                                                                                                                                                                            MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5201
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                                 56
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                         TYPE: nuclei
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CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                          NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
 ATGTTTTTGTTGCCATAATGACAGCCTCTACAACTGTGATAGTCAATTTTTTCTGCAAAT 1869
                               TGCATGGTGCGATTCAGAATT 2348
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Knechtle, Philipp
                                                                                              Conservative
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Steiner, Sabine
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                                                                                                           2.1%;
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 Mismatches

                                                                                                           Score 65.8; DB 4;
Pred. No. 0.00015;
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                                                                                                                          Length 615;
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                                          APPLICATION NUMBER: CH 0016/97
FILLING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Me19s, J. Timothy
REGISTRATION NUMBER: 38, 241
REFERENCE/DOCKET NUMBER: PF/5-30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                        APPLICATION NUMBER: UFILING DATE: 24-DEC-1 CLASSIFICATION: 435 PRIOR APPLICATION DATA:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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Research Triangle Park
No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                            27709
                                919-541-8689
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Knechtle, Philipp
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Steiner, Sabine
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                                                                                                                                                                                                                                              Sequence 651, Application US/09641638 Patent No. 6432648
                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                       TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM FILE REFERENCE: GENSET.0510P1

CURRENT APPLICATION NUMBER: US/09/641;638

CURRENT FILING DATE: 2000-08-16

PRIOR APPLICATION NUMBER: US 09/502,330

PRIOR FILING DATE: 2000-02-11

PRIOR PILING DATE: 2000-02-11

PRIOR PILING DATE: 1999-05-07
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Best Local Similarity
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MOLECULE TYPE: D
ORIGINAL SOURCE:
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            APPLICATION NUMBER: US 09/275,267 FILING DATE: 1999-03-23
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 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                  TAATTAATATTTATCATTATTTAATTAATT 594
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Chumakov, Ilya
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Conservative
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                                      NUMBER: US 60/133,200
1999-05-07
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us 60/119,917
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Pred. No. 0.00018;
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PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
SOFTWARE: Patent.pm
SEQ ID NO 651
LENGTH: 20674
                   NAME/KEY: allele
LOCATION: 1827
OTHER INFORMATION: 10-510-173
                                                                  NAME/KEY: allele
LOCATION: 1570
OTHER INFORMATION:
                                                                                                           NAME/KEY: allele
LOCATION: 1559
OTHER INFORMATION: 10-509-284
                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 17555..20674
OTHER INFORMATION: 3'regulatory region
                                                                                                                                                                                                                                                                                        NAME/KEY: exon
LOCATION: 17063..17554
OTHER INFORMATION: exon
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LOCATION: 16775..16945
OTHER INFORMATION: exon
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ORGANISM: Homo sapiens
                                                                                                                                                          OTHER INFORMATION: 10-508-245
                                                                                                                                                                                                                    NAME/KEY: allele
LOCATION: 1128
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LOCATION: 6349..6509
OTHER INFORMATION: exon
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LOCATION: 1182
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LOCATION: 3124..3297
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OCATION: 16567..16667
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OCATION: 1330
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CATION: 12854..13023
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OCATION: 7379
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OCATION: 5758
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LOCATION: 5552
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OCATION: 8645..8854
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OTHER INFORMATION: NAME/KEY: allele LOCATION: 3802
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NAME/KEY: allele
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OTHER INFORMATION:
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LOCATION: 4170
OTHER INFORMATION:
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NAME/KEY: allele
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                          OTHER INFORMATION:
NAME/KEY: allele
                                                  NAME/KEY: allele LOCATION: 6611
                                                                            OTHER INFORMATION:
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NAME/KEY: allele
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NAME/KEY: allele
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LOCATION: 5903
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NAME/KEY: allele
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OTHER INFORMATION:
NAME/KEY: allele
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NAME/KEY: allele
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LOCATION: 2341
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LOCATION: 2323
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LOCATION: 6183
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  INFORMATION: 10-348-391
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LOCATION: 12429
OTHER INFORMATION: 10-350-332
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OTHER INFORMATION: 10-507-353
NAME/KEY: allele
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LOCATION: 13492
OTHER INFORMATION: 10-507-321
NAME/KEY: allele
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LOCATION: 12171
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LOCATION: 8926
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OTHER INFORMATION: 10-349-224
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LOCATION: 8777
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OTHER INFORMATION: 10-349-142
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LOCATION: 8658
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Best Local Similarity 46.8%;
Matches 278; Conservative
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LENGTH: 8920 base pair
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard
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MEDIUM TYPE: Floppy disk
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2222 TATTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAAATTATATAA 2281
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.24
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O'Sullivan, William J
OENTION: Nucleotide sequence encoding carbamoyl
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 0.00074;
0; Mismatches 304;
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; LENGTH: 8920
; TYPE: DNA
; ORGANISM: Plasmodium falciparum
US-09-150-741-1
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CURRENT APPLICATION NUMBER: US/09/150,741
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: PL6380
EARLIER FILING DATE: 1992-12-16
EARLIER APPLICATION NUMBER: AU93/00617
EARLIER FILING DATE: 1993-12-02
EARLIER FILING DATE: 1993-12-02
EARLIER APPLICATION NUMBER: 08/446,855
EARLIER APPLICATION NUMBER: 08/446,855
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US-09-150-741-1
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Best Local Similarity 46.8%;
Matches 27%; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate Patent No. 6183996
TITLE OF INVENTION: Synthetase II
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1934 AAGACAAAATTTTTGAAAAATGTTATA-ATTTCTAACAATATTATTAAAAATATGATGCCT 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1874 AATTAGGAATTCAATGCTATCAATAGAAGAAACAGCTGAGTATTACATTTTAATTTA 1933
                                                                                                                                                                                                                                                                                                                                                                                                                                            1993 ATAATGTATTTCCTATGTTCTTAAAATAITTTTTTTTATATTTTAGTTATAAATACATTAT 2053
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Pred. No. 0.00074;
0; Mismatches 304;
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PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 199-05-07
PRIOR APPLICATION NUMBER: US 60/137
PRIOR APPLICATION NUMBER: US 60/137
PRIOR APPLICATION NUMBER: US 60/137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM FILE REFERENCE: GENSET.051CP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 20674
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: exon
LOCATION: 3871..4072
OTHER INFORMATION: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: exon
LOCATION: 3124..3297
OTHER INFORMATION: exon
                                                    LOCATION: 8645..8854
OTHER INFORMATION: exon
OTHER INFORMATION: exon
               NAME/KEY: exon
LOCATION: 12254.
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                                                                                                                             NAME/KEY: exon LOCATION: 7379
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LOCATION: 6349..6509
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LOCATION: 5758..5880
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LOCATION: 5552
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LOCATION: 1123..3123
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THER INFORMATION: exon

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NAME/KEY: allele
LOCATION: 2947
OTHER INFORMATION: 10-513-365
NAME/KEY: allele
LOCATION: 3802
OTHER INFORMATION: 12-206-81
NAME/KEY: allele
                                                NAME/KEY: allele
LOCATION: 4109
OTHER INFORMATION: 10-343-278
                                                                                                                  LOCATION: 4062
OTHER INFORMATION: 10-343-231
NAME/KEY: allele
            OTHER INFORMATION: 10-343-339
                         NAME/KEY: allele
LOCATION: 4170
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OTHER INFORMATION: 12-206-366
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LOCATION: 2934
OTHER INFORMATION: 10-513-352
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LOCATION: 2844
OTHER INFORMATION:
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OTHER INFORMATION: 10-513-250
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OTHER INFORMATION: 10-509-284
NAME/KEY: allele
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OTHER INFORMATION:
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LOCATION: 1128
OTHER INFORMATION: 10-508-191 :
NAME/KEY: allele
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OCATION: 2341
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OCATION: 1827
WHER INFORMATION: 10-510-173
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THER INFORMATION: 10-509-295
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OTHER INFORMATION: 10-508-245
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OTHER INFORMATION: 3'regulatory region
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OTHER INFORMATION: exon
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OTHER INFORMATION: exon
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OCATION: 2323
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OCATION: 17555..20674
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CATION: 2048
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Best Local Similarity
Matches 224; Conserv
                                                                           NAME: ...
LOCATION: 13*;
OTHER INFORMATION: 3
TWG/KEY: allele
                                           OTHER INFORMATION: NAME/KEY: allele LOCATION: 13535
                                                                                                                                                                                                                                                                 NAME/KEY: allele
LOCATION: 8785
OTHER INFORMATION:
                                                                                                                                  LOCATION: 13341
OTHER INFORMATION:
                                                                                                                                                                                                 LOCATION: 12171
OTHER INFORMATION:
                                                                                                                                                                                                                                  LOCATION: 8926
OTHER INFORMATION:
                                                                                                                                                                                                                         NAME/KEY: allele
                                                                                                                                                                                                                                                           NAME/KEY:
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                                                                                                                                                                                                                                                                                                                NAME/KEY: allele LOCATION: 8777
                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: allele
LOCATION: 8608
OTHER INFORMATION: 10-349-47
                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: allele
LOCATION: 7668
OTHER INFORMATION:
                                                                                                                                                                    OTHER INFORMATION:
                                                                                                                                                                            OCATION:
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                                                                                                                                                                                                                                                                                                                                                NAME/KEY: allele
LOCATION: 8703
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OTHER INFORMATION:
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LOCATION: 6484
OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 8658
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OTHER INFORMATION:
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LOCATION: 6183
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LOCATION: 6141
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Score 63; DB 4; Length 20674; Pred. No. 0.0012; Indels 1

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PCT/JP96/02597
                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sakai, Y TITLE OF INVENTION: TITLE OF INVENTION:
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                                 PRIOR APPLICATION DATA:
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                                                                                                      APPLICATION NUMBER: PCT/
FILING DATE: 12-SEP-1996
                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 09-MAY-1997
APPLICATION NUMBER: JP 42536/1996 FILING DATE: 29-FEB-1996
                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                     APPLICATION NUMBER:
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Kato, No. 6001590uo
Sakai, Yasuyoshi
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Best Local Similarity 44.4%;
Matches 338; Conservative
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LENGTH: 4818 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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ORIGINAL SOURCE:
ORGANISM: Can
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NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 08
TELECOMMUNICATION INFORMATION:
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             GTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAG
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                                                                                                                                                         TTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAAATTTTGTTAACAGAAACTTCCAAA 2181
                                                                                                                                                                                            TTTGTTTAAATTGGTATACCATTTTTTTTTTTTACTCTATTTACCTATTTAATTTAATTATATA 4618
                                                                                                                                                                                                                              ATAGTTGGTGAATTCAAATATCTCCATTAATATTTTTTTGAAATCTACAAATTATTAATAT 2121
                                                                                                                                                                                                                                                                                                     TTCCTATGTTCTTAAAAATATTTTTTTTTATATTTAGTTATAAATACATTATGAACCAATA 2061
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                                                                                                                     TTATTATCGAAAAAACCTTAAAAAGGACTTCGTAAATTTTATTGTAATAAACGCAAAAA 4678
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Pred. No. 0.001;
0; Mismatches 419;
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                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 209; Conserv
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  1947
                                                                                                                                                            1767 TTTTTTGAAAATGTAACCCTTTTACTCATAGATTAATTACCGTATGTTTTTGTTGCCATA 1826
                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RIG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
FILLING DATE: 02-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: UP FILING DATE: 19920625
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TGAAAAATGTTATAATTTCTAACAATATTATTAAAAATATGATGCCTATAATGTATTTCCT
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                                                                              ATGACAGCCTCTACAACTGTGATAGTCAATTTTTTCTGCAAATATTAAATTAGGAATTCA 1886
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One Liberty Place 46th Floor
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Chang, Andy C M
Williams, Keith L
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Pred. No. 0.0015;
0; Mismatches 217;
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US-09-316-083-2
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US-09-316-083-2
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Best Local Similarity 47.4
Matches 215; Conservative
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SEQ ID NO 2
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EARLIER FILING DATE: 1998-05-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/316,083A
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                      AGCAAATTTTAAAAAATTATATAAAGCCTATACGCGCTCAAAGTATGTTATCTAGTAGGTG 2317
                                                                                                         AACAAGAATAACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGTAATATACATTA
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Pred. No. 0.0014;
0; Mismatches 238;
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US-08-817-926-27
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US-08-817-926-27/c
                                              Query Match
Best Local Similarity 46.3
Matches 275; Conservative
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APPLICANT:
4718 TTTTTTTATTTCTTTTTTTTTTTTTTTATATATGTCATTTTTGCGTTTATTACAATA 4659
                                                                                                                                     MOLECULE TYPE: 1
ORIGINAL SOURCE:
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TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 12-SEP
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                          54 TTCTGGTTATTCTGTTCACATGATTTGAGTTTGGTTCTCAATTTTGGATTCCAAGATAATT 113
                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP 42536/1996 FILING DATE: 29-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/JP96/02597 FILING DATE: 12-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
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/ENTION: PROMOTER/TERMINATOR FOR CANDIDA BOIDINII
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Kato, No. 6001590uo
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                                                                                                                          Candida boidinii
                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                              Stephen A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-MAY-1997
                                                                                                                                                   DNA (genomic)
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                                                   Score 60.8; DB 3;
Pred. No. 0.0023;
0; Mismatches 312;
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                                                                               Length 4818;
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US-08-998-416-288/c
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FILING DATE: 31-DEC-1996 ATTORNEY/AGENT INFORMATION: NAME: Meigs, J. Timothy
                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                           APPLICATION NUMBER: CH 0 FILING DATE: 31-DEC-1996
                                                                                                                              FILING DATE:
                                                                                                                                                APPLICATION NUMBER:
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Research Triangle Park
No. 6239264th Carolina
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Knechtle, Philipp
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Steiner, Sabine
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RESULT 15
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Best Local Similarity 49.1%;
Matches 191; Conservative
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                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Stewar
      ZIP: 22201-4714
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
TYPE: nucleic acid
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                             TITLE OF INVENTION:
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ORIGINAL SOURCE:
ORGANISM: PAG
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                                                                                                      COUNTRY:
                                                                                                                        STATE:
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REFERENCE/DOCKET NUMBER: PF
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TELEFAX: 919-541-8689
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                                                                                                                  Arlington
: Virginia
                                                                                                                                           3: Nixon & Vanderhye PC
1100 No. 5849573th Glebe Road, 8th Floor
                                                                                                                                                                                            Flores, marin.
O'Sullivan, William J
NVENTION: Nucleotide sequence encoding carbamoyl
                                                                                                                                                                                                                                                                    Stewart,
                                                                                                        USA
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Best Local Similarity
Matches 163; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
       8451
                                                               8511
                                                                                                                       8571
                                                                                                                                                                   8631 TATAAAAAAATAAATCAATATAAATTAATGATCATATTTAATAAAAACATTTATTAATAT
                                                                                                                                                                                            2039 TATAAATACATTATGAACCAATAATAGTTGGTGAATTCAAATATCTCCATTAATATTTTT 2098
                                                                                                                                      2099 TGAAATCTACAAATTATTAATATTTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAA 2158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.009
REFERENCE/DOCKET NUMBER: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 8920 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
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AAATACATAAATAAGTAATGTTAAATCGAATTTA 8418
                                                   TATTATATATTACTATTTATATATTTATACTTTTCATGTTGTTATGGAATGAAAGTTAAT 8452
                                                                                                            TTTTGTTAACAGAAACTTCCAAATTTTTTTTTTTTATGGAACAAGAAATAACAGATAGAA 2218
                            AACTATTTTGTTGTGGAATGGAAGTAGTAATATA 2252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
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Pred. No. 0.0031;
0; Mismatches 171;
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Search completed: March 30, Job time: 323.977 secs 2003, 09:01:35

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Result
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Maximum DB
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Sequence:
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                                                                                                                                                                                                                                                                                                                               Score
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65.2
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length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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US-09-774-4114-2

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Sequence 11214, A
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Sequence 11218, A
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54	54	54.2	54.6	54.8	54.8	55.2	55.2	55.2	55.6	55.6	55.8	56.2	57	57.2	57.4	57.4	58.4	58.4	58.4	58.6	58.6	59	59.4	59.4	59.8
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	Segmence 11034 A	Seguence 4527 An	Sequence 4584 An	Sequence 1. Appli	Sequence 6976. Ap	Sequence 13, Appl	Sequence 2868, Ap	Seguence 27 April	Sequence 3 Appli	Sequence 3. Appli	Sequence 2991. An	Sequence 2. Appli	Sequence 3059, Ap	Seguence 3603. An	Sequence 4. Appli	Sequence 6528. An	Sequence 18. Appl	Sequence 3333. An	Segmence 5785 An	Sequence 3 April 1	Sequence 3 Appli	Sequence 3504 An	Sequence 13. Appl		Sequence 154. Ann

ALIGNMENTS

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CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 1
LENGTH: 640681 Matches 395; Query Match
Best Local Similarity GENERAL INFORMATION: Sequence 1, Application US/09790988 Patent No. US20020127687A1 324686 ATATTGTTAGTATTCTTTTTTATATTACCAATATATTTATCATCAATTAATATTTGGCAAC 324745 APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159 TYPE: DNA
ORGANISM: Buchnera 1679 1559 ATATTTATTGTTAGTTGGAATTTAATAAGAGCGAACTTGTAACATTACAATATTTATATT 1618 1619 GCATGAAGGATAAACCTAATGACTTTAATTTTTTGAAAATGTAACCCCTTTTACTCATAGA 1798 AAATCTTTTGTACAAAGAATAAAATATTATTTTTTTTTATCTATAAATCCATTTTTGATC 324805 AGATACTAGTATGTGATTATTCCAAATACATACTTTGGATGTTTAAACTTÄATCTTGTTT 1678 TCTTCTATCATGTAAAAATAATCAATTTCTTTCTTAATATCAATAATTCTTTTAATATAT 324865 CTTCCTACGGTATAAATATTAATCATCGAGGTAAAAAAAGTTTTGTCTTATTTTCGCGAT 1738 Conservative 2.5%; 45.8%; 0, Score 80; DB 10; I Pred. No. 0.0033; 0; Mismatches 455; Length 640681; Indels 12; Gaps

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APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION UNMERR: US/09/960,352
RUMBER OF SEG ID NOS: 15112
SEG ID NO 11218
LENGTH: 424
TYPE: ""
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                                                                                                   ; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 48-LIB3058-026-Q1-K1-D12
US-09-960-352-11218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAATTTGCATCGAATCGATAAAAATAAAAATTTTTATTTTCAATTGAATATATTCAAAACA 325523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTAGTTATAAATACATTATGAACCAATAATAGTTGGTGAATTCAAATATCTCCATTAATA 2093
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                                                Score 66.4; DB 10; Pred. No. 0.038;
                                Mismatches
                                196;
                                Indels
                                                                 424;
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45163)..(45314),(45450)..(45509),(46941)..(48763),(48975)..(49573)
; OTHER INFORMATION: Clone ID: 240017_region_G3
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                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 2
LENGTH: 335913
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 399; Conserv
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                                                                                                                                                                                              279575 ATTAATATAAAAATATTAAAATTATAACATTTTTAAGAAAAATATAACAGTAAATATTAT 279634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 1119
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Glycine max
                                                                                                                                                                                                                               1582 AATAAGAGCGAACTTGTAACATTACAATATTTATATTAGATACTAGTATGTGATTATTCC 1641
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                                                                                                                        TTTAATACAAAAATTCCTCTTTTATTTTTAGTTATTTTTTAAGACAAAGATTAACAT
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                                                                                                                                                                                                                                                                                   2.0%;
                                                                                                                                                                                                                                                                  Score 65.2; DB 9;
Pred. No. 0.67;
0; Mismatches 458;
                                                                                                                                                                                                                                                                                                     Length 335913;
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APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules An
TITLE OF INVENTION: Soybean Cyst Nematode Re
FILE REFERENCE: 38-10(15810)8
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
SEQ ID NO 3
LENGTH: 335913
TYPE: DNA
; FEATURE:
; MAME/KEY: CDS
; LOCATION: (46798)..(48763).(48975)..(49573)
; OTHER INFORMATION: Clone ID: 240017_region_G3
US-09-754-853A-3
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Publication No. US20030005491A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280407 TITAATTACCTGTTAACTAATCAGAA 280432
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APPLICANT: Parnel
                                                                                                     ORGANISM: Glycine max
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Best Local Similarity 46.1%;
Matches 399; Conservative
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                                 ACTATTGAGGGGCAAAAAAAAGACAA 2446
                                                                                               AAAACGGAATTAAAATATTAACTTTAAAATAAATAAAATTTGAGTAAATGTGTTTTCTG
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                                                                                                                                                             ATGTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGAATTCAGAATTGGGACAACAATG 2360
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                                                                                                                                     ATTAGTATTAGTATATTATTATTATATATATATATOCRATATTTTGCATAATAATA
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US-09-969-373-1212/c

Sequence 1212, Application US/09969373 Patent No. US20020133852A1 GENERAL INFORMATION: APPLICANT: Effertz, Roger J.

APPLICANT:

Hauge,

Brian M.

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CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US 09/754,853
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
SEQ ID NO 1212
LENGTH: 473
TYPE: DNA
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                                                                                                          ; OTHER INFORMATION: Clone ID: 48-LIB3058-052-Q1-K1-D8 US-09-960-352-11234
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                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11234, Application US/09960352 Patent No. US20020137139A1
                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 11234
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Best Local Similarity 52.2%;
Matches 166; Conservative
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APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Warren, Wesley C. APPLICANT: Tao, Nengbing
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                                                                                                                                         LENGTH: 419
TYPE: DNA
ORGANISM: Bos taurus
1842 ACTGTGATAGTCAATTTTTTCTGCAAATATTAAATTAGGAATTCAATGCTACTATCAATA 1901
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                                    al Similarity
189; Conser
                                    Conservative
                                                 2.0%;
                                 Score 64.2; DB 10;
Pred. No. 0.086;
D; Mismatches 188;
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; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera s
US-09-790-988-1
                                                                                                                                                            Db 609448
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                                                                                                                                                                                                                                                                                                                                       Db 609568 GTCATTTCTAAATCTATCCAGATTAAATTTTTTTTATTGATTTTTCATATTTTTTCATAAT 609509
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APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.0%;
Best Local Similarity 46.4%;
Matches 327; Conservative
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APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DIA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: JP2000-107160 PRIOR FILING DATE: 2000-04-07 NUMBER OF SEQ ID NOS: 7
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                                                                   TAAAAATTTTTTGATTAGAATATTATTCTAGAAAAATTTAAAATATTTTATATACACA 609329
                                                                                                                                                       TATTAAATATTTTTTTTATTAACATTAAACTTGATTTTAATAAGATAAAAATAGAATTTTT 609449
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                                                                                                           TGTTTTTGTTGCCATAATGACAGCCTCTACAACTGTGATAGTCAATTTTTTTCTGCAAATA 1870
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0; Mismatches 363;
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Pred. No. 1.2;
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; LOCATION: (45163)..(45314),(45450)..(45509),(46941)..(48763),(48975)..(49573)
; OTHER INFORMATION: Clone ID: 240017_region_G3
US-09-754-853a-2
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APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules An
TITLE OF INVENTION: Soybean Cyst Nematode Re
FILE REFERENCE: 38-10(1.5810)8
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION UMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
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Best Local Similarity 47.3%;
Matches 258; Conservative
Sequence 2, Application US/09754853A Publication No. US20030005491A1 GENERAL INFORMATION:
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SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hauge, Brian M. APPLICANT: Parnell, Laure
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                                                                                                LENGTH: 335913
TYPE: DNA
ORGANISM: Glycine max
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                                                                 TAAAATTAATGTTTTCTGGAGCTAAAATTAATAAAACAGAGAATCGTTCTGTTTTACATA 608914
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Pred. No. 1.7;
0; Mismatches 282;
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                                                                                                                                       Db 280434
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; LOCATION: (46798)..(48763),(48975)...(49573)
; OTHER INFORMATION: Clone ID: 240017_region_G3
US-09-754-853A-3
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Best Local Similarity
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SEQ ID NO 3
LENGTH: 335913
                                                                                                                                                                                                    Matches 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09754853A publication No. US20030005491A1 GENERAL INFORMATION:
APPLICANT: Hauge, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Soybean Cyst Nematode
FILE REFERENCE: 38-10(15810)B
                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/754,8:
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
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                                                                                         AATACATTATGAACCAATAATAGTTGGTGAATTCCAAATATCTCCATTAATATTTTTTGAA 2102
                                                                                                                         ATTTCTGATTAGTTAACAGGTAATTAAACTCATAACGAATATAATAATAATTATAATAATA 280375
                                                           AGGTTT 279893
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Pred. No. 1.7;
0; Mismatches 282;
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US-09-754-853A-1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/754,853A CURRENT FILING DATE: 2001-01-05 PRIOR APPLICATION NUMBER: US 60/174,880 PRIOR FILING DATE: 2000-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With TITLE OF INVENTION: Soybean Cyst Nematode Resistance FILE REFERENCE: 38-10(15810)B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 1119
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APPLICANT:
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AA--ATTATTATTATTTGTTTATATAGATTAAAATTGATCTATATGAATATTTTAAAA 71721
                                                                                                                                                                AACGATTTTTCTTGGATTCCATTCAATGATCTAAAATGCATAGATCTTTTGGGTTACAGT 1490
                                  TCTTTAACATATTTATTGTTAGTT----GGAATTTAATAAGAGCGAACTTGTAACATTACA 1607
                                                                  TATAAATTATTGATTATTTTTTATTGTTGTTCAATTTTAATAAAAATTTGATTCAAATGA 71781
                                                                                               GGGTTT 2466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAATTATATCTGATTCGATATTTTATACGCATCAAAATTATATAGGATTAGAGTTTATT 279899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang, Ming Li
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                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                 1.9%;
43.5%;
                                                                                                                                                                                                                                                                                 Score 62.2; DI Pred. No. 1.5;
                                                                                                                                                                                                                                                                 Mismatches 493;
                                                                                                                                                                                                                                                                                                DB 9;
                                                                                                                                                                                                                                                                                                Length 127197;
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: NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PATENTIN Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3410
; TYPE: DNA
; ORGANISM: Tetrahymena thermophila
US-10-196-063-1
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  Query Match
Best Local S
Matches 305
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Publication No. US20030027192A1
GENERAL INFORMATION:
APPLICANT: GOFOVSKY, Martin A.
                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/196,063
CURRENT FILING DATE: 2002-07-15
PRIOR APPLICATION NUMBER: 60/305,167
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: 60/317,322
PRIOR FILING DATE: 2001-09-05
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Shang, Yuhua APPLICANT: Song, Xiaoyuan TITLE OF INVENTION: TETRAHYMENA METALLOTHIONEIN GENE PROMOTER AND ITS FILE REFERENCE: 176/61102
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    Local Similarity hes 305; Conserv
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                  1.98;
Score 61.6; DB 9;
Pred. No. 0.49;
0; Mismatches 359;
                                       Length 3410;
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      TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION (UMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 4756
                                                                                                                                                                                                                                                                                      Sequence 4756, Application US/09938842A Patent No. US20020160378A1 GENERAL INFORMATION:
                                                                                                                                                                                                                    APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
LENGTH: 1713
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; LOCATION: (1)..(1428; US-09-774-414-2
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US-09-774-414-2
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Query Match
Best Local Similarity
Matches 215; Conserv
                                                                                                                                                                                    SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09774414
Patent No. US20020102231A1
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Best Local Similarity 46.6%;
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                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/774,414
CURRENT FILING DATE: 2001-01-31
                                                                                                                                                                                                                                                                                                   FILE REFERENCE: PH-651
                                                                                                                                                                                                                                                                                                               APPLICANT: The Institute of Physical and Chemical Research TITLE OF INVENTION: Endonuclease
                                                                                                                                                                                                 SOFTWARE: PatentIn
                                                                                                                                     LENGTH: 1431
TYPE: DNA
ORGANISM: Saccharomyces
                                                                                       NAME/KEY: CDS
LOCATION: (1)
                                                                                                                       FEATURE:
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ORGANISM: Arabidopsis thaliana
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Pred. No. 0.41;
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US-09-962-832-154
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SEQ ID NO 154
LENGTH: 302250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/962,832
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/60/235,077
PRIOR FILING DATE: 2000-09-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 259
SOFTWARE: Date: 259
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                                                                                                                   300182
                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US/60/235,280
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les 166; Conserv
ATTTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAATTTTGTTAACAGAAACTTCCA 2179
                                       TAATAGTTGGTGAATTCAAATATCTCCATTAATATTTTTTGAAATCTACAAATTATTAAT 2119
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RESULT 15
US-09-938-842A-3532/c
Sequence 3532, Application Useront No. US20020160378A1
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PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 3532
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CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
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APPLICANT: Kreps, Joel
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AATAAATGATTTTTTTAGTAATTCTTATGTTAAATATTAG 412
                                                                                                             ATACATTAAGCAAATTTTAAAAAATTATATAAGCCTATACGCGCTCAAAGTATGTTATCT 2309
                                                                                                                                                      GTAATATAATTTAAATTTTTACTATAAAATAAATAAATGTTTTGAAGAGAAATTTATAAT
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                                                                           TATGAATTTATTTTAAATTAGTATAAATAAATGTTTTAAAGTGAAATTTATTTTAAATTT 572
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Search completed: March 30, 2003, 13:11:02 Job time: 4203.88 secs

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ALIGNMENTS

RESULT 1
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ORGANISM JOURNAL REFERENCE JOURNAL REFERENCE AUTHORS TITLE REFERENCE AUTHORS TITLE JOURNAL TITLE AUTHORS thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer 3 (bases 1 to 473)
Li,Y., Rosso,M., Strizhov,N. and Weisshaar,B.
Direct Submission Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H. Unpublished and Weisshaar, B. AL768954 473 bp L Arabidopsis thaliana T-DNA flanking genomic survey sequence. AL768954 Unpublished AL768954.1 GI:21522073 DNA DNA linear GSS 18-JUN sequence GK-082A08-011867, GSS 18-JUN-2002

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237; Conserv
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                                            1 (bases 1 to 148)
Alonso, J.M., Leisse, T.J., Barajas, P.,
                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Sosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                      BH811044 148 bp DNA linear GSS 02-MAY-20 SALK_057128 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_057128, DNA sequence.
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  Karnes,M., Kim,C.J., Parker,H.,
and Ecker,J.R.
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Pred. No. 1.5e-18;
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                                         ROSSO,M., Strizhov,N., Li,Y., Reiss,B., Dekker,n. and meccanical A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10010 N. Torrey Pines Road,
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                    SS9
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Class: TDNA tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
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                                                                                                                                                         Unpublished
                                                                                                                                                                                (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines
                                                                                                                                                                                                                          A pipeline for automated high-throughput generation of FSTs
                                                                                                                                                                                                                                                   and Weisshaar, B
                                                                                                                                                                                                                                                                      Strizhov, N., Li, Y., Rosso, M., Viehoever, P.,
                                                                                                                                                                                                                                                                                                                                                                                                           thale cress.
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llarity 100.0%;
Conservative
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Rosso, M.,
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/clone="PCR was performed on Arabidopsis thaliana lines.
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
a 28 c 14 g 60 t
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Length 148; Indels

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Gaps

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Dekker, K., Saedler, H.

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RESULT 4
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                                                                                                                        JOURNAL
                                                                                                                                                                       AUTHORS
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                                                                                                                                                                                              Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
Pphydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                       fly), ger
AL069706
                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster genome sur
BACR29B23 of RPCI-98 library from
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as collaboration with the Berkeley Drosophila Genome Project The BDGP is constructing a physical map of the Drosophila
                                                                                            Submitted (02-JUN-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                                                       Genoscope
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                                                                                                                                                 Direct Submission
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/clone=lib="Arabidopsis thaliana T-DNA insertion lines"
/clone=lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thalaina nuclear genome sequence were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   processed for submission. T-DNA derived sequences were removed "

58 c 70 g 146 t 31 others
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rom Drosophila melanogaster (fruit
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                                    2224 TTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAA 2271
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/db_xref="taxon:7227"
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Matches 223; Conserv
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 AAATTAGGAATTCAATGCTACTATCAATAGAAGAAGAACAGCTGAGTATTACATTTTAATTT 1932
                                                                                               TTTTTGTTGCCATAATGACAGCCTCTACAACTGTGATAGTCAATTTTTTTCTGCAAATATT 1872
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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1097 AMAMAMCMAWTÄTHTTTHAAACTCIMTTHTTTTMTTTYTMTMTTCTCTTTTTTTTTTTTTT 1038
                                                   1748 ATAAACCTAATGACTTTAATTTTTTGAAAATGTAACCCCTTTTACTCATAGATTAAATTACC 1807
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

[ (bases 1 to 1101)
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    Web : www.genoscope.cns.fr)

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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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/db_xref="taxon:7227"
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                                                                                                                                           43.98;
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Pred. No. 1.
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Drosophila melanogaster genome survey sequence I/ ENGLE CILLER BACN05N18 of DrosBAC library from Drosophila melanogaster (fruit flv), genomic survey sequence.
                                                                                                                                                                                                                                           - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EBGF)-http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                       Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP) The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and malanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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AV717372 DCB Homo sapiens
AV717372
   ř
               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 807)
                                                                 Homo sapiens
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EST.
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                                                                                    human.
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/db_xref="taxon:7227"
/clone="BACR29P01"
/clone_lib="RPCI-98"
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Liu, F.,
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Qu,J., Zhao,M.,
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Pred. No. 5.3e-05;
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 Li,Y.,
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 Huang, Q.,
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 Zhou, J.,
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CCAAATTTTTTTTTTTTTTTTGGAACAAGAAATAACAGATAGAAAACTATTTTGTTGTGGAA 2236
                                                                                                                               CAATAATAGTTGGTGAATTCAAATATCTCCATTAATATTTTTTGAAATCTACAAATTATT 2116
                                                                                                                                                                                             ATTAAGTCAAATTTTATTTTTTTATGTTTATTATTACTTATTGGATAATAATATAAGGTC
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                                                                                            TGTATTTCCTATGTTCTTAAAATATTTTTTTTTATATTTAGTTATAAATACATTATGAAC 2056
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                                                               AATAGAAACTCCTATAGAAAAAGATAAATGAATATAATAAATTAATAATTATACGTATTTG
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201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
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Contact: Zeguang H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ,G., Cheng,Z. and Han,Z.
Homo sapiens cDNA DCB clones
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clone is available at CHGC
Location/Qualifiers
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/lab_host="BM25.8"
/note="Vector: pTriplEx2;
50 c 20 g 345
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/clone_lib="DCB"
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                                                                          ATTCAATGCTACTATCAATAGAAGAAACAGCTGAGTATTACATTTTAATTTAAAGACAAA 1941
                                                                                                                                                   ATTTWTAAAWTWTTTTAAAWAATTATTTWWTTTTTTAWTAAWTAAAWTNTTTTWTTTAAA 807
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Tetraodon nigroviridis genome survey sequence T7 end of clone
222L11 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roest-Crollius, H., Jaille
Bouneau, L., Billault, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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2 (bases 1
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1 (bases 1 to 1092)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="222L11"
                                                                                                                                                                                                                                                                                                                                                                                          /Clone_lib="G"
/Clone_lib="G"
/note="Genoscope sequence ID : COAG222CF06LP1-end : T7"
/note="Genoscope sequence ID : COAG222CF06LP1-end : T7"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
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 TTTATWTATAAAWAWAWTTTTTTYWTTAAAAAAAAAWTTAAAAATWTAAAAATTATAAA
 Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila
 AL064091
 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08K08 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
 Direct Submission
 Drosophila melanogaster.
 (bases 1 to 1101)
 Conservative
 GI:4941847
 2.9%;
 87; Mismatches 303;
 Score 94;
Pred. No.
 DB 17;
0.0002;
 Length 1201;
 525
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 Indels
 Pterygota;
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 1722 TGTCTTATTTTCGCGATGCATGAAGGATAAACCTAATGACTTTAATTTTTTGAAAATGTA 1781
 1782
 1062
 642
 762
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 942
 Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial isogenic strain y2; on bw sp. the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be libraries. A more detailed description of the library of filters for hybridization from the BACPAC Resource Center can be libraries.
 GAAGAAACAGCTGAGTATTACATTTTAATTTAAAGACAAAATTTTTGAAAAATGT-----
 AAATATCTCCATTAATATTTTTGAAATCTACAAATTATTAATATTTAGTCAATAAAAA 2136
 TATAATTTCTAACAATATTATTAAAATATGATGCCTATAATGTATTTCCTAAGTCTTAA 2016
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 AAAWAAWTAWTTWATTTTTATWTTAATTTTTTTTTTWTTAWTTTAWTTATTTWAAAWWTAT
 ACTGTGATAGTCAATTTTTTCTGCAAATATTTAAATTAGGAATTCAATGCTACTATCAATA 190
 ATTTTTTTTTWWTATTATAATWATWATATAAAAAATATTWTWTWTAATWRWTTTWTARAK
 ACCCTITTACTCATAGATTAATTACCGTATGTTTTTGTTGCCATAATGACAGCCTCTACA 1841
 TNTADTIKTTTTTKWTATRWATAKAWTTTTTWGTRIWTTRTWWTWTWNATTTWATTTT 1003
 Drosophila melanogaster genome sur
BACR29P01 of RPCI-98 library from
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Drosophila melanogaster
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 51;
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Pred. No. 0.00024;
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 DB 17;
 149 others
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 2165 TAACAGAAACTTCCAAATTTTTTTTTTTTTTGGAACAAGAAATAACAGATAGAA----- 2219
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 1866 AAATATTAAATTAGGAATTCAATGCTACTATCAATAGAAGAAACAGCTGAGTATTACATT 1925
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 485
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 Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo NY. The library is named RPCJ-98 and was constructed by partial isogenic strain v2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACBAC Resource Center can be found at http://www.med Parkship.com/files.
AATGWTTTWTAAATTWWGTTAWTTTTTATTTTWAAATTGTATATAAAAAWWATTATGTA
 TWYTTTTWTTTAWITTAAWATTTTTTTAWWTAAWAWTGTAATWAAATTAWWTAAAAW
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 GATGCCTATAATGTATTTCC-TATGTTCTTAAAATATTTTTTTTTATATTTTAGTTATAAA 2044
 ACATKAAWAAARRGGGGAKAAATAWTTKGAAAGATATAAAAAAAAAATAAWTAAWATTAA 484
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 Direct Submission
 Genoscope
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 at http://bacpac.med.buffalo.edu/drosophila_bac.htm
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/organism="Drosophila melanogaster"
/olone="acr2901"
/clone_lib="Repc1-98"
/note="end: TET3"
a 66 c 104 g 351 t 214 ot
 Location/Qualifiers
 2.9%; Score 93.6; DB 17
40.4%; Pred. No. 0.00024;
 Mismatches 269; Indels
 DB 17;
 214 others
 Length 1101;
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 1036
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 1809 TATGTTTTTGTTGCCATAATGACAGCCTCTACAACTGTGATAGTCAATTTTTTCTGCAAA 1868
 source
 960
 Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the 1990 and EST libraries. A more detailed description of the library or filters for hybridization from the BACQPC Resource Center can be found at http://bacne.med.html
ATTTAAAGACAAAATTTTTGAAAAATGTTATAATTTCTAACAATATTATTAAAATATGAT 1988
 TATTAAATTAGGAATTCAATGCTACTATCAATAGAAGAAACAGCTGAGTATTACATTTTA 1928
 CGGGTTTGA 2468
 TAWWAAATRTWWTGTATTKAAAATATWGRATATTKAAAAAAAAAAATAWTAAAAWARTKKT 1019
 TWATTAATATWATTTTTAAAAAAAATWAAAWTTWTTTAATTWAAATTTTTAAATWTTTT 977
 GTRTWTKWA 1028
 υνοsophila melanogaster genome survey sequence T7 end of BAC #BACR24D09 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL057419
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr | Web : www.genoscope.cns.fr |
 Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
 Direct Submission
 Drosophila melanogaster.
 AL057419.1 GI:4937885
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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 melanogaster"
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564 ATTAAAARSATAARAAATTAKTRAAAAAATATTTTGTKGTKGTTTTTADTTWDWTTA 506
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 TTTASTSSATAATTATTSVTRATTGVTTDAWTTTAAARSAAAAAWKTTTRBAAAAAAA 565
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Listing first 45 summaries
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<pre>1 (bases 1 to 4818) Choe,S., Dilkes,B.P., Fujioka,S., Takatsuto,S., Sakurai,A. and</pre>	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	Arabidopsis thaliana	Arabidopsis thaliana.		AF044216.1 GI:2935341	AF044216	complete cds.	Arabidopsis thaliana steroid 22-alpha-hydroxylase (DWF4) gene,	AF044216 4818 bp DNA linear PLN 25-JUN-2001		

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Plant Cell 10 (2),
 Submitted (22-JAN-1998) Plant Sciences, University of Arizona,
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 The DWF4 gene of Arabidopsis encodes a cytochrome P450 that mediates multiple 22alpha-hydroxylation steps in brassinost
 The DWF4 gene
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pe/S., Dilkes, B.P., Azpiroz, R. and Feldmann, K.A.
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 on Jan 27, 2000 this sequence version replaced g1:6434247.
Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.blochem.mpg.de/proj/thal/.
 lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de project coordinator: Marcel Salanoubat and Francis Quetier, Groupemer d'Interet public, Centre National de Sequencage - GENOSCOPE; Gaston Cremieux, BP191, 91006 Evry Cedex, France;
 Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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1 (bases 1 to 84196)
Bloecker, H., Mewes, H.W., Lemcke, K., Mayer, K.F.X., Quetler, F. and
 Submitted (25-JAN-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-m
 http://www.genoscope.cns.fr
 Direct Submission
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 Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.I., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R. W., Theologis, A. and Ecker, J.R.
 1 (bases 1 to 1691)
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2 Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A. D., Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Marusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Yamamura, Y., Tu, G., Yu, S., Shinozaki, K., Yanaha, R., Theologis, A. and Ecker, J.R.
sequencing and annotation of the RAFL cDNAs: Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Shinn,P., Banh,J. Bowser,L., Dale,J.M., Goldsmith,A.D., Jiang,P.X., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Yamada,K., Yamaura, Y., Yu,G., Yu,S., Davis,R.W., Theologis,A., and Ecker,J.R.
 RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAs (RAFL CDNA: 'RIKEN Arabidopsis Full-Length CDNA'): Seki,M., Narusska,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
 Submitted (21-AUG-2001) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
 The Salk, Stanford, PGEC (SSP) Consortium members carried out
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to

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 Length 7560;
 immune system
 HTG 13-JUL-2002
IN PROGRESS
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 PAT 01-FEB-2002
 297
 237
 5315
 63
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 REFERENCE
AUTHORS
 TITLE
.JOURNAL
REFERENCE
AUTHORS
TITLE
 COMMENT
 KEYWORDS
SOURCE
 REFERENCE
 JOURNAL
 TITLE
 JOURNAL
 AUTHORS
 ORGANISM
 Cleveland, C., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C., D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagy, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Jac, M., Hodges, M., Holloway, C., Hollins, B., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kartson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kartson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Loudson, R., Lucier, A., Lucier, R., Luna, R., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Massey, E., Martiney, E., McLeod, M.P., Meador, M., Mei, G., Metzker, M., Moser, M., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Rives, J., Tohers, A., Tohers, S., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Wang, J., Welson, R., Wang, O., Williamson, A., Wallalamson, A., Wallalanson, R., Wang, O., Watlington, S., Warden, S., Warden, R., Wang, O., Watlington, S., Warden, A., Wallams, G., Watlington, S., Warren, R., Wand, O., Watlington, S., Wallams, O., Wallas, M., Thomas, N., Thomas, N., Thomas, N., Thomas, N., Thomas, N., Thomas, S., Wallamson, A., Wallamson, A., Wang, O., Watlington, S., Wallamson, A., Wallamson, A., Wallamson, S., Wallamson, S., Wallamson, A., Wallamson, S., Wallams
 Submitted (23-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
 Worley, K.C.
Direct Submission
 of Molecular and Human
Baylor Plaza, Houston,
3 (bases 1 to 173786)
 Worley, K.C.
Direct Submission
 Unpublished
 Direct Submission
 Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
 Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 Center project name: GNJF
center clone name: CH230-29B17
Sequencing vector: Plasmid;
 Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Project Information
 (bases 1 to 173786)
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Dye-terminator Big Dye: 100% of reads
 Bonnin, D.,
Bryant, N.P.,
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "vorking draft' sequence. It currently consists of 92 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
 as soon as it is available and the accession number will be preserved.
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27954

VERSION KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

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MUZNY, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Blouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Burch, P., Burch, P., Burkett, C., Burrell, K.L., Byd, N.C., Chavez, D., Chen, G., Chen, R., Cavazos, S.R., Chacko, J., Chavez, D., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Devila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Bouthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Falls, T., Ferrayuto, D., Flagg, N., Brd, J.C., Escotto, M., Falls, T., Ferrayuto, D., Flagg, N., Brd, J.C., Escotto, M., Falls, T., Ferrayuto, D., Flagg, N., Brd, J.C., Escotto, M., Gabisi, A., Gao, J., García, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hawes, A., Hernandez, J., Homsi, F., Howard, S., Huber, J., Hully, S., Hame, J., Jackson, L.E., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., King, T., Houle, S., Harlins, B., Jay, Y., Johnson, R., Jolivet, S., Joudah, S., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Locado, R.J., Lui, X., Lucier, A., Lucier, R., Luna, R., Martinez, E., Massey, E., Mawhiney, E., McCiecol, M.P., Martindale, A., Martinez, E., Miner, G., Martinez, E., Necteod, M.P., Martindale, A., Martinez, E., Miner, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stoop, H., Wang, R., Wang, H., Sonaike, T., Sparks, A., Stanley, H., Stoop, R., Wang, H., Wang, S., Watch, A., Tabor, P., Tamerisa, K., Tamas, S., Walfon, R., Warfen, R., Warfen, R., Wang, S., Watchon, R., Wang, H., Wang, S., Watch, A., Tabor, P., Tamerisa, R., Tamerisa, K., Tamas, S., Walfon, S., Watch, S., Walfon, R., Wang, G., Watch, S., Walfon, D., Wang, R., Worley, K., Wolley, K.,
 Direct Submission

Submitted (12-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2002 this sequence version replaced gi:20066030.
 Submitted (24-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 309233)
Worley, K.C.
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Direct Submission
 Wu,C., Wu,Y., Wu,Y.F., Zh
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 Unpublished
 Direct Submission
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 Mammalia; Eutheria;
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 AC098557.6 GI:21728854
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 GHJV
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 61 contigs. The true order of the pieces
is not known and their order in this sequence record is
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This record will be updated with the finished sequence
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 NOTE: Estimated insert size may differ from sequence length
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REFERENCE AUTHORS

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COMMENT

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Score Pred.

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REFERENCE
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Ax251264
 artificial sequences.
1 (bases 1 to 12356)
Olek, A., Piepenbrock, C. and Berlin, K.
 Olek, A., Piepenbrock, C. and Berlin, K. Diagnosis of diseases associated with the Patent: WO 0200928-A 1625 03-JAN-2002;
 synthetic construct. synthetic construct artificial sequences.
 Diagnosis of diseases associated with tumor suppressor genes and
 synthetic construct
 Epigenomics AG (DE)
 Patent:
 synthetic construct.
 AX251264.1 GI:15984687
 AX251264
 Epigenomics AG (DE)
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 1562
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 WO 0168912-A 232 20-SEP-2001;
 232 from Patent
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 (Homo
 PAT 05-OCT-2001
 sapiens)"
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 Gaps
 3410
 243
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 COMMENT
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 ORGANISM
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 9231 ATTITATICTACTITICATTICTATTTTTTCATCATCAATC 9272
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 131 TTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTAGGTT 190
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On Aug 12, 2000 this sequence version replaced g1:8810447.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the places
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 Similarity
 Submitted (19-FEB-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto,
 2 (bases 1 to 169546)
Hyman,R.W., Qin,F., Fung,E.L., Conway,A.B. and Davis,R.W.
Direct Submission
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Hyman, R.W., Fung, E.L., Qin, F., Rowley, D.,
Kurdi, O.B., Conway, A.B. and Davis, R.W.
Plasmodium falciparum 3D7 chromosome 12
 Unpublished
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HTG; HTGS_PHASE1.
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 (Homo
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DNA

linear.

PAT

02-NOV-2001

GI:16608755

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 Biotechnology, Beutenberstr. 11, Jena 07745, Germany CDS predictions from GeneID may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis
 Submitted (04-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany
 Gloeckner,G., Eichinger,L., Szafranski,K., Pachebat,J., Dear,P., Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
 Dictyostelium discoideum.
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
 AC116967

Dictyostelium discoideum chromosome 2 ma
AX4, *** SEQUENCING IN PROGRESS ***, in
 Olek, A., Piepenbrock, C. and Berlin, K. Diagnosis of diseases associated with metastasis Patent: WO 0177376-A 164 18-OCT-2001;
 synthetic construct.
synthetic construct
 Direct Submission
 Sequence and Analysis of Chromosome 2 of Dictyostelium
 Noegel, A.A.
 HTG; HTGS_PHASE2
 AC116967
AC116967.1 GI:19920066
 Epigenomics AG (DE)
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(http://genome.imb-jena.de/dictyostelium/)
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 04-APR-2002
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 REFERENCE
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 Agency: Deutsche Forschungsgemeinschaft (DFG).

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
 Epigenomics AG
 Patent:
 Diagnosis
 synthetic
 AX344570.1
 rtificial sequences.
 and the Univerity Colonge, Institute for Biochemistry (http://www.uni-koeln.de/dictyostelium/project.shtml
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 PAT 01-FEB-2002
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REFERENCE
AUTHORS
TITLE
 RESULT 15
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1 (bases 1 to 133280)

Gloeckner, G., Elchinger, L., Szafranski, K., Pachebat, J., Dear, Lehmann, R., Baumgart, C., Parra, G., April, J.F., Gulgo, R., Kumg Tunggal, B., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A. and
 Biotechnology, Beutenberstr. 11, Jena 07745, Germany CDS predictions from GeneID may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis
 Submitted (06-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany
 Dictyostelium discoideum.
Dictyostelium discoideum
 Dictyostelium discoldeum chromosome AX4, *** SEQUENCING IN PROGRESS ***,
 Submitted (21-MAY-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany
 Direct Submission
 Baumgart, C.
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 Baumgart,C.
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 Noegel, A.A.
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http://www.uni-koeln.de/dictyostelium/project.shtml
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 (bases 1 to
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2.149.980-seq 21 2.10
2.749.980-seq 23 2.70
3.349.980-seq 25 3.30
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* NOTE: This is a 'working draft'
* This sequence will be replaced
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 Deutsche Forschungsgemeinschaft (DFG)
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/db_xref="GI;21039741"
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P 64 B

YQ i

Db

CDS

CDS

CDS

CDS

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 CDS
 121 TTAGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATAT 173
 Local
 61 TTTTTTTGCCCAATGATATAAAAAATTTGGATAAATAATATTATTGGATATTCGTTTT 120
 99;
 Similarity
 Conservative
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Maximum DB seq
 Total number of hits satisfying chosen parameters:
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 Sequence:
 Title:
Perfect score:
 OM nucleic - nucleic search, using sw model
 Post-processing:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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358
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Maximum Match 100%
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 GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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5926
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AAA59599
ABL33641
ABL33223
ABL33652
AAS436510
ABL32028
ABL32028
ABL34611
ABL34127
ABK28455
 SUMMARIES
 4370478
 DNA encoding a cyt
Human immune syste
Human immune syste
Human immune syste
 Description
 Tumour suppressor
Human immune syste
Human metastasis a
 Human immune syste
 DNA encoding
 cell updates/sec
 358
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	FFFEX OXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	
cDS exon intron exon intron	RESULT 1 AAA59599 ID AAA59 XX AAA59 XX AAA59 XX L14-NO XX DNA e XX DWF4; XX DWF4; XX Plant XX Plant XX Promo	44444488888888888888888888888888888888
on on	9599 9599; 9599; OV-20 Ov-20 encod encod encod	### ##################################
\@\@\@\@\\\ \@\@\&\\\\\\\\\\\\\\\\\\\\\	ndard (fir a cy a cy pe; sp. L	11111111111111111111111111111111111111
3203.6100 3203.6100 **tag= c /*tag= c /*tag= c /*tag= c /*tag= d 3424.350 3424.350 **tag= e 3504.3828 /*tag= g	DNU 150 bch	14147 14147 5678 5678 64118 6418 66115 16750 6145 17131 13506 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 13606 1360
3 <b>a</b>	888 888 P4 Pua	00000000000000000000000000000000000000
DWF4" tains introns"	ALIGNMENTS  3P.  Denzyme designate brassinosteroid; lon; ss.	AAS46743 ABK33955 ABK33955 ABL33138 ABL19002 ABL33138 ABL32551 ABL32551 ABL32551 ABL32615 ABL33053 ABL33019 ABL32742 ABL33742 ABL33744 ABL33746 ABL32849 ABL32849 ABL32849 ABL32849 ABL32849 ABL32849 ABL32849 ABL32849 ABL32849 ABL33936 ABL33175 ABL7333 ABK28280 ABL735144 ABL34175 ABL49336 ABL795244 ABL34175 ABL49336 ABL795246 ABL33218 ABR49336 ABL33218 ABR49336 ABL33218 ABR3936 ABL332218 ABR3936 ABL332218 ABR3936 ABL332218 ABR3936 ABL332218 ABR3936 ABL332218 ABR3936 ABL332218 ABR3936 ABL33226 ABL79526 ABL79526
	d DWF4. 22alpha-hydroxylation;	Tumour suppressor Tumour suppressor Tumour suppressor Human immune syste Human immune syste Drosophila melanog Human immune syste DNA transcription Tumour suppressor Human immune syste Chemically m Human immune syste Human immune syste

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exon

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 Query Match
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Matches 358
 6171
 The present sequence encodes a DWF4 polypeptide. The polypeptide is a cytochrome P450 enzyme that mediates multiple steps in synthesis of brassinosteroids. Specifically, it mediates multiple 22alpha-hydroxylation steps in brassinosteroid biosynthesis. The DWF4 polynucleotide is used for altering the phenotype of a plant. DWF4 plants display a dramatic reduction in the length of different organs, and this size reduction is attributable to a defect in cell elongation. The DWF4 polynucleotides and polypeptides can be used in diagnostic assays and to generate antibodies, which can be used to produce
 6111
 exon
 exon
 Sequence
 Claim 3;
 New isolated dwf4 polynucleotide useful plants, for diagnostic assays and in the
 11-FEB-1999;
11-FEB-1999;
 11-FEB-2000;
 17-AUG-2000
 3'UTR
 exon
 (ARIZ-) ARIZONA BOARD OF REGENTS
 WO200047715-A2
 intron
 intron
 exon
 immunogenic compositions.
 intron
 intron
 121
 61
 TTAGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGG
 TTTTTTTGCCCAATGATATATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTT
 2000-549142/50.
DB; AAB07921.
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 358;
 Similarity
 8889
 Fig 10A-G; 113pp; English.
 Conservative
 Choe
 2000WO-US03820
 B₽;
 990S-0119657.
990S-0119658.
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6011..6468
 /*tag= q
5865..6110
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4480..4631
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5111..5864
 /*tag= m
4816..4894
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4632..4724
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4725...
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 2294 A;
 100.0%;
 ..4815
 ..5000
 Feldmann
 1010
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 Score 358; I
Pred. No. 3.2
); Mismatches
 Š
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 1193
 the
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 for altering the production of an
 DB 21;
.2e-55;
 2391 T;
 0
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 Indels
 Length 6888;
 other;
 he phenotype antibodies -
 0;
 Gaps
 6230
 120
 180
 of.
 0;
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Matches Query Match Best Local

85;

Conservative

0

Pred. No. 0.09 ); Mismatches Score

58;

DB

.053;

45;

Indels

0

Gaps

0

63

Similarity

16.2%;

Sequence 5449

BP; 1146 A; 90 C;

1299 G;

2914 T; 0 other;

including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myelo; leukaemia, Alzheimer's disease, ADDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.

The present invention provides a number of human immune syst genes which are modified by the methylation of cytosines. The can be used in the diagnosis and treatment of immune system can be used in the diagnosis and treatment of immune system.

immune system associated

acute myeloid

disorders,

sequences

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HINGE STATE OF THE RESULT 2
ABL33641
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 Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
 6411
 6291
 6231
 Claim 1; SEQ ID NO 1614; 32pp + Sequence Listing;
 Nucleic acid comprising for diagnosis and treatm
 30-JUN-2000;
01-SEP-2000;
 antiinflammatory; cancer; eye disease; arteriosclerosis; acute myeloid leukaemia; Alzheimer's disease; AIDS; epile
 02-JUL-2001; 2001WO-EP07537
 03-JAN-2002
 WO200200928-A2.
 Homo sapiens.
 gene;
 neurofibromatosis; rheumatoid arthritis;
 26-MAR-2002
 ABL33641,
 ABL33641 standard; DNA; 5449
 (EPIG-)
 .241
 301
 2002-130909/17.
 AACTTTTACTTCGTTTTTGATCCGAAGCAATAACAAATTGTCAAATACCAAACACAAG
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 AACTTTTACTTCGTTTTTGATCCGAAGCAATAACAAATTGTCAAATACCAAACACAAG
 ATTAAACCTTAAATGGGCTTTCTATAAGGCCCCAATTATATTACGATTATAACAAAGTGAC
 as
 immune
 EPIGENOMICS
 methylation
 Piepenbrock
 2000DE-1032529
2000DE-1043826
 (first entry)
 system
 treatment
 å
 associated
 fragment of chemically modified ment of diseases associated with
 Berlin
 ВP
 gene
 7
 SEQ
 IJ
 psoriasis; bowel
 ŏ:
 German.
 epilepsy
 abnormal
 gene,
 anaemia;
 disease;
 6410
 6350
 300
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RRESULT 3

ID ABL3:

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XX
 Matches
 Query Match
Best Local
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 Ъ
 2728
 Sequence 7560 BP; 2154 A; 47 C; 1554 G;
 The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
 diseases.
 Claim 1; SEQ ID NO 1196;
 leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
 Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation -
 30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
 02-JUL-2001; 2001WO-EP07537
 (EPIG-)
 antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirhoumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
 W0200200928-A2
 Homo sapiens.
 gene;
 Human; immune system disease; cytosine methylation; antiasthmatic;
 neurofibromatosis;
 Human immune
 ABL33223;
 ABL33223 standard; DNA; 7560
 5256
 124
 64
2002-130909/17.
 TTTTGGGTTT 5385
 GTTCGGGTTT
 TTTTTGCCCCAATGATATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTA 123
 Similarity
 EPIGENOMICS
 The
 Piepenbrock C,
 present sequence is a gene of the
 system associated gene SEQ ID NO: 1196.
 (first entry)
 133
 16.2%;
 Æ
 rheumatoid arthritis; psoriasis; bowel dis
 32pp + Sequence Listing; German.
 Berlin
 0,
 Score 58;
Pred. No.
 Pred. No. 0.05
0; Mismatches
 7
 DB
 3805 T;
 .053;
 24;
 145;
 0 other;
 Length 7560;
 invention
 Indels
 disease
 4;
 Gaps
 5315
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Sequence 5926 BP;

1562 A;

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2991 T; 0

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 The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
 macular degeneration, arteriosclerosis, anaemia, cancer, acute mys leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/nlocketing to the control of the
 Claim 1; SEQ ID NO 1625; 32pp + Sequence Listing; German.
 01ek
 cytosine
 Nucleic acid comprising fractor diagnosis and treatment
 Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
 (EPIG-) EPIGENOMICS
 30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
 02-JUL-2001; 2001WO-EP07537
 03-JAN-2002.
 WO200200928-A2
 Human immune system associated gene SEQ ID NO: 1625
 Homo sapiens
 26-MAR-2002
 ABL33652;
 ABL33652 standard;
 3028
 2968
 2908 TATTATTAAATTAATTTGATAAATAGTAATAAATGTGTGATGTATGTTATTTTTAAATTT
 2848
 2788
 298
 238
 182
 122
 62
 2002-130909/17.
 GACAACTT 305
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 GATAAATT 3035
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 TTTTATTGTGGAGTTATTTTAAATTTTTAAGGATAATTTTATTTTTATGTCGTGTTATTT
 TTTTTTTTGCCCAATGATATAAAAATTTTGGATAAATAATATTATTGGATATTTTT
 TGTTTTGTATTATAAAAATTATTTTAGGATTTTTTATTTGTATTTTAAAAATAAAATTAT
 methylation
 Piepenbrock C,
 The present sequence is
 (first entry)
 ĀG
 DNA; 5926
 psoriasis and inflammatory/ulcerative sequence is a gene of the invention.
 fragment of chemically modified ment of diseases associated with
 Berlin
 7
 i gene, us
abnormal
 acute myeloid
 useful
 2967
 2907
 181
 2847
 121
 237
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DB 24;

Length 5926;

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RESULT 5
AAS46510
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 Matches 159;
 Query Match
Best Local
 06-APR-2000;
07-APR-2000;
30-JUN-2000;
The invention relates to a nuclero
 Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; cytosine methylation; ds.
 3471
 3411
 3291
 3231
 3171
 analysing
 Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for
 Claim
 WPI; 2001-602752/68
 15-MAR-2001;
 WO200168912-A2
 Homo sapiens.
 Tumour suppressor gene derived
 AAS46510
 (EPIG-)
 15-MAR-2000;
 304
 184
 124
 64
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 TATGAGATATTAAGTTTAGGAAGAAGAAGATTTTTGGAATGGAAATATTTTTGGGTG
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 TTTTTGCCCCAATGATATATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTA 123
 AAACCTTAAATGGGCTTTCTATAAGGCCCCAATTATATTACGATTATAACAAAGTGACAAC
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 EPIGENOMICS AG
 SEQ ID No 232; 27pp; English.
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 Piepenbrock
 diseases
 2000DE-1013847.
2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
 Conservative
 2001WO-EP02955
 (first entry)
 associated
 15.8%;
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 12356
 a nucleic acid
 Berlin
 0;
 Score
Pred.
 n designing primers and probes
with cytosine methylation stat
 chemically modified sequence #232
 Mismatches 171;
 pretreated DNA (CP
 56.4;
No. 0.
 333
 Indels
 sequence of 18 DNA) e.g. with
 state e.g.
 0
 SNP
 3470
 3410
 3350
 3290
 303
 3230
 183
 0;
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WO200200928-A2

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RESULT 6
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 Š
 CC bisulphite, of genes associated with tumour suppression and CC oncogenes having a sequence taken from 536 (actually 533 since CC numbers 408, 458 and 500 are missing from the sequence listing) sequences CC (SS) and sequences complementary to (SS). The nucleic acid may be a CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may CC form part of a set of probes for detecting the cytosine methylation state CC and/or single nucleotide polymorphisms and also to be used in an CC array for analysing diseases associated with CpG dinucleotides e.g. CC cancers and tumours. The probes can also be used in amethod for CC cancers and tumours. The probes can also be used in a method for CC cancers and funders and of the concert of the diagnosis CC and/or therapy of existing diseases or the predisposition to specific CC diseases, by analysing cytosine methylations. The parameters may be CC compared to another set of genetic and/or epigenetic parameters, the CC differences serving as basis for diagnosis and/or prognosis events which CC are disadvantageous to patients. The present sequence is one of the CC 33 genomic sequences derived from tumour suppressor genes and CC complementary sequence of the corresponding odd numbers are the CC complementary sequence of the corresponding odd numbers depuence (e.g. In part of the corresponding odd numbers are the correspondence (e.g. In part of the corresponding odd numbers are the correspondence of th
 Matches 118;
 Query Match
Best Local S
 9231
 9051
 gene;
 antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute_myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
 Human; immune system disease; cytosine methylation; antiasthmatic;
 Human
 26-MAR-2002
 ABL32028 standard;
 Sequence 12356
 of the printed specification, but was obtained format directly from WIPO at
 HOMO
 neurofibromatosis;
 neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
 antiarteriosclerotic;
 ABL32028
 ftp.wipo.int/pub/published_pct_sequences
 Note: The sequence data for this patent
 is missing).
 191
 131
 11 AGATGAAAGTATTTTTATTCTCTTCTTTTTTTTTTGATAATTTTAAATCATTTTTTTGC
 71
 sapiens
 ATTTTATTGTAGTTTTGATTTGTATTTTTTTGATGATTAATG 9272
 TTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTAGGTT
 GAGTCTTTGGACATTTGTATTGGATGTTGTTGATTATTAGTG
 CCAATGATATATAAAAATTTGGATAAATATTATTGGATATTCGTTTTTTAGTTCGGG 130
 g
 immune system associated gene SEQ
 Similarity 53.:
18; Conservative
 (first entry)
 BP;
 DNA;
 rheumatoid
 3645 A; 68 C; 2127 G; 6516 T;
 15.5%;
53.2%;
 antianaemic; cytostatic; nootropic;
 0,
 Score 55.6; DB Pred. No. 0.14;
 eimer's disease; AIDS; arthritis; psoriasis;
 Mismatches 104;
 Ħ
 did not
 Š.
 22;
 in electronic
 form part
 0 other
 Indels
 Length 12356;
 epilepsy;
bowel dis
 disease;
 0,
 Gaps
 9230
 9170
 9110
 0
```

2001WO-EP07537.

```
RESULT 7
ABL3451
ID ABL3
XX
AC ABL3
XX
DT 26-M
XX
DE Huma
XX
DE Cytc
XX
Cytc
XX
DS Homo
XX
DS Homo
XX
DS MO20
 밁
 ρy
 В
 Qy
 Дb
 δÃ
 밁
 Ϋ́
 밁
 Ş
 밁
 Š
 Query Match
Best Local :
 Matches
 WO200177376-A2
 Homo sapiens
 cytosine methylation;
 Human metastasis associated
 Metastasis associated gene;
 4065
 4005
 3945
 26-MAR-2002
 ABL34611;
 ABL34611 standard; DNA;
 3885
 3825
 The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
 Sequence
 320
 260
 200
 Claim 1; SEQ ID NO 1; 32pp + Sequence Listing; German.
 Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with cytosine methylation
 140
 Olek A,
 30-JUN-2000;
01-SEP-2000;
 WPI; 2002-130909/17.
 (EPIG-)
 80
 TTTAATAAGAATGTAAAATTTTTAAGT
 ATCCGAAGCAATAACAAATTGTCAAAT 346
 TTCTATAAGGCCCAATTATATTACGATTATAACAAAGTGACAACTTTTACTTCGTTTTTG
 AATAATATGTTTGGTTATTGTATTTTATATGTAGTTTTATATTGTATTTTTATATTGTAT
 GACATTTGTATTGGATGTTGTTGATTATTAGTGTCGACACTATTAAACCTTAAATGGGCT 259
 TATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTAGTTCGGGTTTGAGAAA 139
 AGGTTTTAGGTTTGGGTTATGTGTTTTTTTATGTGTTTTTAGAGTATTTTGAATTTTTGT 3944
 AGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTAGGTTGAGTCTTTG 199
 al Similarity
157; Conserv
 7351 BP; 2230 A; 42 C; 1230 G; 3849 T; 0 other;
 EPIGENOMICS AG
 Piepenbrock
 Conservative
 (first
 2000DE-1032529.
2000DE-1043826.
 15.4%;
 entry)
 gene;
 Ç
 20486
 Berlin
 cytostatic;
ds.
 gene SEQ
 0;
 Pred.
 Score 55;
Pred. No.
 ВP
 Mismatches 170;
 ζ.
 A
 0.18;
 gene therapy; cancer;
 NO: 164
 DB 24;
 Length 7351;
 Indels
 gene, useful
abnormal
 0;
 Gaps
 4004
 319
 3884
 0
밁
 Ş
 Ş
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RESULT 8
 ₽
 밁
 QΥ
 뫄
 γ
 В
 Ωy
 밁
 δÃ
 Query Match
Best Local 9
 Matches
Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antiposoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
 12134
 12074
 11896
 12016
 Human immune system associated gene SEQ ID NO:
 26-MAR-2002
 ABL34127;
 ABL34127 standard;
 06-APR-2000;
07-APR-2000;
30-JUN-2000;
 Sequence 20486 BP; 6101 A; 360 C; 4446 G; 9577
 The present invention provides a number of human metastasis associated genes which are modified by cytosine methylation. The sequences can be used in the diagnosis and treatment of cancer. The present sequence is one of the genes of the invention.
 317
 197
 137
 Claim 1; SEQ ID NO 164;
 New nucleic acid derived useful for diagnosis of c
 WPI;
 Olek A,
 also for treatment
 (EPIG-)
 01-SEP-2000;
 06-APR-2001;
 18-OCT-2001
 77
 TTGATCCGAAGCAATAACAAATTGTCAAATACCAAACACAA
 TTTATGTTAÄAAAATATAAATTATTTTAATTTGAAATTAAA
 GATATAAAATGATTTATCGGTAATAAGTATTAAAATAAGATTAAAAATTTTAATTTGTTT 12133
 TTAGGAGTTTTAATAGTTATTAGTTTAGTAGAGATGAGATTAAAATAAATA - - TAAATTT
 TTGGACATTTGTATTGGATGTTGTTGATTATTAGTGTCGACACTATTAAACCTTAAATGG
 GCTTTCTATAAGGCCCCAATTATATTACGATTATAACAAAGTGACAACTTTTACTTCGTTT
 AAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTAGGTTGAGTCT 196
 AFATATAAAAATTTGGATAAATAATATTTGGATATTCGTTTTTTAGTTCGGGTTTGAG 136
 169;
 2002-010922/01.
 Similarity
 EPIGENOMICS
 Piepenbrock
 (first
 Conservative
 2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
 2001WO-EP03970
 DNA;
 entry)
 15.4%;
 å
 c,
 2814
 23pp + Sequence Listing;
 cancers
 from chemically treated metastasis cancers by analysis of cytosine methers.
 Berlin
 ₽₽
 0;
 Score 55; DB 2
Pred. No. 0.17;
 Mismatches
 ~
 DB 24; Length 20486;
 170;
 357
 T; 2 other;
 English
 Indels
 methylation,
 2;
 316
 256
 12015
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RESULT 9
ABK28455
XXXXXXX
 Ş
 ₽
 δÃ
 밁
 ₽
 밁
 δÃ
 밁
 Š
 Matches
 Query Match
Best Local
 The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, ADDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psorlasis and inflammatoryVulcerative bowel diseases. The present sequence is a gene of the invention.
 DNA transcription
 Sequence 2814 BP; 629 A; 144 C; 770 G; 1271 T; 0 other;
 ABK28455
 Claim 1;
 cytosine
 Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
 01ek
 30-JUN-2000;
01-SEP-2000;
 02-JUL-2001; 2001WO-EP07537
 03-JAN-2002
 gene;
 acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
 WO200200928-A2
 Homo sapiens.
 (EPIG-)
 183
 123
 243
 260
 200
 140
 63
 80
 20
 w
 TTCTATAAGGCCCAATTATATGGATTATAACAAAGTGACAACTTTTACTTCGTTTTT 318
 TATTITIATTCICTICTITTITTTTGATAATITTTAAATCATITTTTTTGCCCAATGATA 79
 GACATTTGTATTGGATGTTGATTATTAGTGTCGACACTATTAAACCTTAAATGGGCT
 ATGTATATGTTATATATATGTTATGTGTGTGTATATACGTTTTTTGTATAAACGTTTATA
 AGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTAGGTTGAGTCTTTG 199
 TACGTGTAGGTGGATATATTTTTTTTTTTTATATTTTCGTGTATATGTAAATTTTTTGTAT
 TATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTAGTTCGGGTTTGAGAAA 139
 2002-130909/17.
 146;
 as.
 Similarity
 EPIGENOMICS AG
 standard;
 SEQ ID NO 2100; 32pp + Sequence Listing; German.
 methylation
 Piepenbrock C,
 Conservative
 (first entry)
 2000DE-1032529.
2000DE-1043826.
 associated genomic DNA #165
 DNA;
 15.1%;
 7138
 Berlin
 0;
 Score 54.2;
Pred. No. 0
 Mismatches
 . 26;
 DB 24;
 153;
 Length
 Indels
 gene, useful
abnormal
 0;
 Gaps
 259
 122
 62
 242
 0;
```

```
DNA transcription associated gene; peptide nucleic acid; PNA-oligomer; PNA; cytosine methylation state; SNP; retroviral infection; gene; ds; single nucleotide polymorphism; adenosine deaminase deficiency; cancer; viral infection; Sezary syndrome; haematological disorder; tuberculosis; immunological disorder; Werner syndrome; developmental disorder; psoriasis; Rieger's syndrome; neurological disorder; erythropolesis; neurodegenerative disorder; Waardenburg syndrome; Niemann-Pick disease; myelodysplastic syndrome; myocardial infarction; hypertension; arthritis; angiogenesis; congenital heart disease; HDR syndrome; gene therapy; polyglutamine disorder; solid tumour.
```

Unidentified

WO200192565-A2

06-DEC-2001

06-APR-2001; 2001WO-EP03973

06-APR-2000; 2000DE-1019058 07-APR-2000; 2000DE-1019173 30-JUN-2000; 2000DE-1032529 01-SEP-2000; 2000DE-1043826

(EPIG-) EPIGENOMICS AG

01ek

Piepenbrock

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Berlin

<u>...</u>

BASSASSAS CON CONTRACTOR CONTRACT

New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, soltumours or cancer

Claim SEQ ID No 329; 32pp; English.

The invention relates to a nucleic acid, which comprises a segment of the CC chemically pretreated DNA of genes associated with DNA transcription from one of 346 sequences, and an oligomer, in particular an oligomuclectide one of 346 sequences, and an oligomer that hybridises to or is identical transcription. The set of oligomer that hybridises to or is identical transcription. The set of oligomer probes are useful for detecting the CC cytosine methylation state and/or single nucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleic acids are useful for CC diagnosing or treating diseases associated with DNA transcription CC (particularly with the methylation status), e.g. ademosine deaminase CC deficiency, viral infection, retroviral infection, Sezary syndrome, CC tuberculosis, developmental disorders, psoriasis, Rieger's syndrome, neurological disorders, neurodegenerative disorders, Waardenburg CC syndrome, Niemann-pick disease, myelodysplastic syndrome, mycoardial cc infarction, hypertension, angiogenesis, erythropoiesis, congenital heart CC disease, HDR syndrome, arthritis, polyglutamine disorders, Solid tumours or cancer. Sequences ABX28127-ABX88472 represent DNA transcription CC associated genomic DNA molecules of the invention.

CC Note: The sequence data for this patent did not form part of the printed constitution to the sequence of the invention of the printed constitution in the constitution of the printed cons European Patent Office.

Sequence 7138 BP; 1564 A; 288 C; 1759 G; 3527 T; 0 other

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δÃ 片 Qy Query Match Best Local Matches 3163 w al Similarity 153; Conser Conservative 15.1%; 0; Score 54; Pred. No. Mismatches DB 2 0.27; 24; Length 7138; 165; 0; Gaps

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RESULT 10
AAS46743
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 Qy
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 밁
 The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid complementary to (Ss). The nucleic acid may be a peptide nucleic acid complementary to (Ss) and sequences for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for association and/or therapy of existing diseases or the predisposition to specific diseases by analysing diseases or the predisposition to specific
 Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state {\rm e.g.}
 WPI;
 Olek
 06-APR-2000;
07-APR-2000;
 Human; tumour suppressor gene; cancer; tumour; CpG dinucleotic cytosine methylation; ds.
 Tumour suppressor
 AAS46743 standard;
 3463
 3403
 3343
 3283
 Claim
 01-SEP-2000;
 15-MAR-2001; 2001WO-EP02955
 20-SEP-2001
 WO200168912-A2
 18-DEC-2001
 AAS46743;
 (EPIG-)
 15-MAR-2000;
 Homo sapiens
 303
 243
 183
 123
 ۶
 ATTTTTATAGTTTTTAA 3480
 CTTTTACTTCGTTTTTGA 320
 TAAACCTTAAATGGGCCTTTCTATAAGGCCCCAATTATATTACGATTATAACAAAGTGACAA
 GCTAGGTTGAGTCTTTGGACATTTGTATTGGATGTTGTTGATTATTAGTGTCGACACTAT
 AGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGA
 1; SEQ
 EPIGENOMICS
 Piepenbrock
 2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
 (first entry)
 ID No 467;
 2000DE-1013847
 uppressor gene; oncogene; antitumour; cytostatic; CpG dinucleotide; single-nucleotide polymorphism; atlon; ds.
 gene
 DNA;
 ĀG
 Ç
 derived
 27pp; English
 14147
 Berlin
 ВP
 chemically
 <u>.</u>
 modified
 sequence
specific may be
 SNP;
 302
 3402
 3342
 182
 242
```

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RESULT 11
ABK33955
ID ABK33
 QV
 닭
 δõ
 δÃ
 밁
 δõ
 밁
 Ş
 88888888888
 В
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 밁
 밁
Query Match
Best Local
 Matches
 11111
 11051
 10871
 10991
 10931
 differences serving as basis for diagnosis and/or prognosis events where are disadvantageous to pattents. The present sequence is one of the 533 genomic sequences derived from tumour enormance.
 Note: The sequence data for this patent did not of the printed specification, but was obtained iformat directly from WIPO at
 WPI; 2002-171649/22
 30-JUN-2000;
01-SEP-2000;
 matrix
 Human; ds; a
bisulphite;
 Human DNA for staging
 ABK33955;
 ABK33955
 Sequence 14147 BP;
 oncogenes.
 02-JUL-2001; 2001WO-EP07538.
 10-JAN-2002.
 WO200202808-A2
 18-JUN-2002
 ftp.wipo.int/pub/published_pct_sequences
 (EPIG-)
 187
 127
 307
 67
 7 AAAAAGATGAAAGTATTTTATTCTCTTTTTTTTTTTTTGATAATTTTAAATCATTTTTT
 P,
 TTATTATTATTTGA 11124
 CGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTA 186
 sapiens
 TACTTCGTTTTTGA
 CCTTAAATGGGCTTTCTATAAGGCCCCAATTATACGATTATAACAAAGTGACAACTTT
 GGTTGAGTCTTTGGACATTTGTATTGGATGTTGTTGATTAGTGTCGACACTATTAAA
 TTGCCCAATGATATAAAAATTTGGATAAATATATTATTGGATATTCGTTTTTTAGTT
 151;
 ds; astrocytoma; cytostatic; staging; cysteine methylation;
hite; brain tissue; MALDI; ESI; electron spray mass spectrom
assisted laser desorption/ionization mass spectrometry.
 Similarity
 EPIGENOMICS
 standard;
 Piepenbrock
 Conservative
 (first entry)
 2000DE-1032529
2000DE-1043826
 3621 A;
 DNA;
 320
 g
 14.98;
 ú
 of Astrocytomas #20.
 14147
 Berlin
 225 C;
 0;
 Score 53.2;
Pred. No. 0
 ВP
 Mismatches
 3116 G;
 .36;
 7185
 DB 22;
 163;
 Ŧ;
 in
 form
 0
 electronic
 Indels
 Length 14147;
 other
 part
 0
 Gaps
 306
 246
 126
 66
 10990
 10930
 11050
 which
 0
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Novel chemically modified

genomic

DNA sequences,

useful

in the

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 В
 cc genomic DNA fragments using the array and a polymerase, where the campilficates carry a detectable label. The method further involves cidentifying methylation status of the cytosine positions, and cc analysing methylation status of the cytosine positions by reference to come or more data sets. The genomic DNA is chemically treated by using a complifies DNA which is of particular interest in astrocytoma or cc step amplifies DNA which is of particular interest in astrocytoma or cc tissues, based on the specific genomic methylation status of brain ctissues, as opposed to background. The amplificates carry a cc fluorescent label or radionuclide. Optionally, the labels of the cc amplificates are detachable molecule fragments having a typical mass which are detected in a mass spectrometer. The fragments of chemically createred genomic DNA to be amplified, have a single positive or negative charge for a better detectability in the mass spectrometer. Cc preferably, the amplificates or fragments of the amplificates are detected by matrix assisted laser desorption/ionization mass spectrometry (MALDI) or using electron spray mass spectrometry (ESI). The resembles of the invention
 Matches
 10871
 10811
 10931
 for determining genetic and/or epigenetic parameters, classification, differentiation, grading, staging, treatment and/or diagnosis of astrocytomas, or the predisposition to astrocytomas by analysing cytosine methylations, involves obtaining a biological sample containing genomic DNA, extracting the genomic DNA, converting cytosine bases which are unmethylated at the 5-position, in the genomic DNA sample, to uracil or another base which is dissimilar to cytosine in terms of hybridisation behaviour, by chemical treatment and amplifying chemically pre-treated
 acid (or set thereof) of at least 9 nucleotides which hybridises to (I), primers for (I), probes for detecting cytosine methylation or single-nucleotide polymorphisms (SNP) in (I), an array of oligomers or peptide nucleic acids for analysing diseases associated with the methylation states of the CpG dinucleotides of (I). The array is useful
 Sequence 14147 BP; 3621 A; 225 C;
 of the printed specification, but was format directly from WIPO at
 astrocytomas
 characterisation, classification, differentiation, grading, staging, treatment and/or diagnosis of astrocytomas or predisposition to
 ftp.wipo.int/pub/published_pct_sequences
 samples of the invention.
Note: The sequence data for this patent did not form
 complement.
 DNA which has
 127
 67
 GGTTGAGTCTTTGGACATTTGTATTGGATGTTGTTGATTATTAGTGTCGACACTATTAAA 246
 CGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTA 186
 TTGCCCAATGATATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTAGTT 126
 CCTTAAATGGGCTTTCTATAAGGCCCCAATTATATTACGATTATAACAAAGTGACAACTTT 306
 Similarity
 SEQ ID No
 Also included are an oligonucleotide or peptide
 Conservative
 relates to a nucleic acid comprising a sequence () s in length of a segment of chemically pre-treated any one of the sequences of (ABK33919-ABK34032) or
 relates to a nucleic acid
 39;
 14.9%;
 37pp;
 0
 Score 53.2;
Pred. No. 0.
 English.
 Mismatches
 3116 G;
 obtained in
 . 36;
 7185 T; 0 other;
 DB 24;
 163;
 Indels
 Length 14147;
 orm part
electronic
 0;
 nucleic
 or
C
 (I) of
 1) of at
 Gaps
 LLS
 11050
 10990
 0
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RESULT 12
AAS46670
 밁
 11111 TTATTATTATTGA 11124
 15-MAR-2000; 2000DE-1013847.
06-APR-2000; 2000DE-1019058.
07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
 Claim 1;
 Fragments
genes and
 Tumour suppressor gene derived chemically modified sequence #392
 WO200168912-A2
 cytosine methylation; ds.
 Human; tumour suppressor gene; on cancer; tumour; CpG dinucleotide;
 18-DEC-2001
 AAS46670;
 AAS46670 standard;
 (EPIG-)
 Homo sapiens.
 15-MAR-2001; 2001WO-EP02955
 307
 TACTTCGTTTTTGA
 EPIGENOMICS
 SEQ ID No
 Piepenbrock
 of chemically modified genes associated with tumour suppressor oncogenes, useful in designing primers and probes for diseases associated with cytosine methylation state e.g.
 (first
 392; 27pp; English.
 DNA; 7261 BP
 entry)
 Ç
 Berlin
 oncogene; antitumour;
 single-nucleotide polymorphism;
 SNP;
```

The invention relates to a nucleic acid comprising a sequence of 18 CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with CC bisulphite, of genes associated with tumour suppression and CC oncogenes having a sequence taken from 536 (actually 533 since CC numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may CC form part of a set of probes for detecting the cytosine methylation state CC and/or single nucleotide polymorphisms and also to be used in an CC cancers and tumours. The probes can also be used in a method for CC ascertaining genetic and/or epigenetic parameters for the diagnosis CC and/or therapy of existing diseases or the predisposition to specific CC diseases, by analysing cytosine methylations. The parameters may be CC compared to another set of genetic and/or pigenetic parameters, the CC differences serving as basis for diagnosis and/or prognosis events which care disadvantageous to patients. The present sequence is one of the

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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electro format directly from WIPO at

ftp.wipo.int/pub/published\_pct\_sequences

533 genomic sequences derived from tumour suppressor genes and oncogenes. Sequences with even numbered Seq ID numbers are the complementary sequence of the corresponding odd numbered sequen ID 2 and ID1, ID 536 and ID 535, except for those whose partner

odd numbered sequence those whose partner se

(e.g

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S

S

вP;

1862 A; 171 C; 1854 G; 3374 T; 0 other;

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 В
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 ₽
 δÃ
 Query Match
 01ek
 genes which
 Claim 1;
 including eye diseases such as retinopathy,
 30-JUN-2000;
01-SEP-2000;
 cytosine methylation
 Nucleic acid comprising frag
for diagnosis and treatment
 WPI;
 (EPIG-)
 02-JUL-2001;
 antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
 W0200200928-A2
 Homo sapiens.
 Human immune system associated gene SEQ ID NO: 1111
 neurofibromatosis;
 antiinflammatory; cancer; eye disease; arteriosclerosis;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epil
 26-MAR-2002
 ABL33138
 6467
 6407
 133
 present invention provides a number of human immune system associated es which are modified by the methylation of cytosines. The sequences be used in the diagnosis and treatment of immune system disorders,
 73
 13
 Local
 2002-130909/17.
 TTTGTTTTTTTT
 ATGGGCTTTCTAT
 TTTTTTTTTTATTGGTTTGTTGATTTTGTTGAAGAAAGTTTTGAATTTTAGGTTTTGA
 GTCTTTGGACATTTGTATTGGATGTTGTTGATTATTAGTGTCGACACTATTAAACCTTAA
 TGTAGGAATAAATAAGAGTGTGGGATTTTGTGAGTGTGGATAATGTTATAGGTAAAGGGA
 TGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTAGGTTGA
 AATGATATATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTAGTTCGGGTT
 immune system disease; cytosine methylation; antiasthmatic;
 EPIGENOMICS
 SEQ ID NO 1111;
 Piepenbrock C,
 standard;
 Similarity
 2000DE-1032529
2000DE-1043826
 2001WO-EP07537.
 (first entry)
 Conservative
 6659
 DNA; 5678 BP
 Ą
 265
 14.8%;
 fragment of chemically modified ment of diseases associated with
 32pp +
 Berlin
 0;
 Score 53;
Pred. No.
 Sequence Listing;
 <u>.</u>7.
 Mismatches
 0
 psoriasis; bowel
 DB 22; Length 7261;
 .41;
neovascular glaucoma and
 125;
 German.
 Indels
 epilepsy;
 gene, useful abnormal
 anaemia;
 disease;
 0;
 Gaps
 6526
 132
 6586
 192
 0
```

sequence

data

for this patent did

not form

part of the printed

is

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·Ωγ
 밁
 밁
 Ş
 δÃ
 RESULT 14
 밁
 В
 Š
 Matches
 Query Match
 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elicidating cell signalling and insections in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
 Claim 1; SEQ ID NO 8479; 21pp + Sequence Listing; English
 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cel
 Venter
 23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
 (PEKE) PE
 23-MAR-2001; 2001WO-US09231
 Drosophila melanogaster genomic polynucleotide SEQ ID NO 8479.
 3488
 Drosophila melanogaster.
 pharmaceutical;
 WO200171042-A2
 Drosophila;
 ABL19002;
 ABL19002
 3428
 3368
 26-MAR-2002
 3308
 macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
 Sequence 5678 BP; 1387 A; 32 C; 1284 G;
 216
 156
 96
 36 TTTTTTTTTGATAATTTTAAATCATTTTTTTTGCCCAATGATAATAAAAATTTTGGATA
 ocal
 2001-656860/75.
 TATGTTGATTTTTTTTTTTG
 GTTGTTGATTATTAGTGTCG
 TAATTTTATTATTTTTTTATTATTTTGATTGGGTAATTTTAAATGATTTGTATTTGAG
 AAAGTGGACGATGTATATAGATTGGGAGCTAGGTTGAGTCTTTGGACATTTGTATTGGAT 215
 AATAATATTATTGGATATTCGTTTTTTAGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCG
 JC,
 108;
 standard; DNA; 21231
 Similarity
 CORP NY
 Adams M,
 developmental biology; cell signalling;
 (first entry)
 Conservative
 gene;
 Ŀ
 14.7%;
 PWD,
 3507
 235
 0;
 Pred. No. 0.44
); Mismatches
 Score 52.8; DB
 ВP
 Myers
 EW;
 2975 T; 0 other;
 92;
 24;
 Indels
 Length
 insecticide
 0;
 cell-cell
 Gaps
 155
 3427
 3367
 95
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RESULT 15
ABL32322
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Best Local
 Matches
 16810
 17110 CATCGATTTTCTATTTCAAATGGAAATTGTAAAATCCTTACGAATTCGATTAAC 17164
 16990
 16870
 antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
 Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
 Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
 WPI; 2002-130909/17
 Olek A,
 specification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct_sequences.
 30-JUN-2000;
01-SEP-2000;
 02-JUL-2001; 2001WO-EP07537.
 03-JAN-2002.
 WO200200928-A2
 Homo sapiens.
 gene;
 neurofibromatosis;
 26-MAR-2002
 ABL32322 standard; DNA; 6418
 Sequence
 (EPIG-)
 181
 301
 241
 121
 61
 AACTTTTACTTCGTTTTTGATCCGAAGCAATAACAAATTGTCAAATACCAAACAC
 GCCAGACCAAAAGTGTCCGTTTTACGAATCGAAAAAATTTTACGATTTTGAAAAAACGAAG
 ATTAAACCTTAAATGGGCCTTTCTATAAGGCCCCAATTATACGATTATAACAAAGTGAC
 AAATAATTTTTTCACCTTTGTAAATAAGATCTGATTTAATATAAAAAAGGTCATTATTTCG
 GAGCTAGGTTGAGTCTTTGGACATTTGTATTGGATGTTGTTGATTATTAGTGTCGACACT
 GAAAAAAATTTTTTAAAAGTGTTTTATTTATTTGGAAAATGTATGCTTTAAATAATTTGT 16989
 TTAGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGG 180
 ATATATAAAGAAATATATATATTTATTTTAAACAATGTATGCTTATATAATCAGTTT
 TTTTTTTTGCCCCAATGATATAAAAAATTTGGATAATAATATTATTGGATATTCGTTTT
 immune system associated gene SEQ ID NO:
 EPIGENOMICS AG
 Similarity
methylation
 21231 BP;
 Piepenbrock
 Conservative
 2000DE-1032529
2000DE-1043826
 (first entry)
 6727 A; 3859 C; 3768 G; 6877
 rheumatoid arthritis;
 14.7%;
 Ó
 Berlin
 0;
 ВP
 Score 52.6;
 Pred. No.
 Mismatches
 6; DB 23;
0.46;
 psoriasis;
 189;
 T;
 Length 21231;
 Indels
 0 other;
 epilepsy;
bowel dis
 disease;
 0;
 355
 Gaps
 240
 120
 17109
 17049
 16929
 0;
 . ,
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138.508

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 В
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Search completed: March
 Matches
 Query Match
Best Local
 1230
 1170
 1110
 The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, theumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
 Sequence 6418 BP; 1842 A; 47 C; 1423 G; 3106 T; 0 other;
 diseases. The present sequence is a gene of the invention.
 Claim 1;
 138
 18
 78
 AAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTA
 TAATTGGATTTATTTTTGTTAGGGGGATAATTTATTATGGTTTTTATTTA
 TATATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTAGTTCGGGTTTGAGA 137
 96;
 Similarity
 SEQ
 Conservative
 Ħ
 NO 295; 32pp + Sequence Listing;
29,
 14.6%; 56.8%;
 2003, 19:00:18
 ;0
 Score 52.2;
Pred. No. 0
 Mismatches
 .57;
 DB
 24;
 73;
 German
 Length
 Indels
 1278
 186
 6418;
 0
 Gaps
 0
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Minimum DB:
Maximum DB:
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 Title:
Perfect score:
 OM nucleic -
 Result
 Scoring table:
 Total number of hits satisfying chosen parameters:
 O
 O
 0000000
 0000
 ŏ
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 39.4
39.4
39.4
 40.8
40.6
40.6
 nucleic search, using sw model
 length: 0
length: 2000000000
 Issued_Patents_NA:*
1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
 US-09-502-426A-1_COPY_6111_6468
 Query
Match Length DB
 IDENTITY_NUC Gapop 10.0 , Gapext 1.0
 March 29, 2003, 18:09:40; Search time 12.5196 Seconds (without alignments) 8769.450 Million cell updates/sec
 441362 seqs, 153338381 residues
 aaaaaaaaaaaagatgaaagt.....tgtcaaataccaaacacaag 358
 GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
 /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
 1 US-08-340-820-24

US-08-593-535-24

US-09-122-400B-5

US-09-056-075-1

US-09-056-075-1

US-09-073-569-1

15-231168-1

US-08-749-522-2

US-08-341-568-3

US-08-341-568-3

US-08-341-568-3

US-08-341-568-3

US-08-487-826B-13

US-08-487-826B-13

US-08-487-826B-13

US-08-98-416-547

US-08-98-416-547

US-08-98-416-24

US-08-98-416-22

US-09-055-051-26

US-09-055-051-26

US-08-098-416-701

US-08-98-416-701

US-08-98-347-221B-24

US-09-005-051-26

US-09-005-051-26

US-09-0134-001C-2606

US-08-9134-001C-2606
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 SUMMARIES
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Sequence 24, Appli
Sequence 5, Appli
Sequence 1, Appli
Sequence 1, Appli
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Sequence 1, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 13, Appli
Sequence 14, Appli
Sequence 4, Appli
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Sequence 27, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 266, Appli
Sequence 266, Appli
Sequence 2667, Appli
Sequence 2667, Appli
Sequence 2667, Appli
Sequence 2667, Appli
 Description
 Patent No.
 TOPOLOGY:
 ADDRESSEE:
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45	44	<b>4</b> 3		41	_	39	_			35	-		32	31	30	29	28
37.2	37.4	37.4	37.4	37.4	37.4	37.6	37.6	37.6	37.6	37.6	37.8	37.8	38	38	38	38	38
10.4	10.4	10.4	10.4	10.4	10.4	10.5	10.5	10.5	10.5	10.5	10.6	10.6	10.6	10.6	10.6	10.6	10.6
144	10223	3761	2674	2445	477	6078	5852	3138	2422	2107	1582	1582	8700	8700	8700	2555	2555
1	4	4	4	σ	4	4	<b></b>	<u></u>	۳	4	w	w	N	N	N	4	2
US-08-702-344-26	US-08-961-527-73	US-08-890-865A-2	US-09-817-180-1	5215909-9	US-08-887-534A-81	US-09-173-914-1	US-07-867-106-2	US-07-867-106-4	US-07-867-106-5	US-09-180-852-1	US-08-545-196B-12	US-08-545-196B-10	US-08-645-193B-18	US-08-466-961A-16	US-08-392-625-16	US-09-265-731-3	US-08-693-457-3
Sequence 26, Appl	Sequence 73, Appl	'n	Sequence 1, Appli	Patent No. 5215909	Sequence 81, Appl	Sequence 1, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 5, Appli	Sequence 1, Appli	•	Sequence 10, Appl	Sequence 18, Appl	Sequence 16, Appl	Sequence 16, Appl	Sequence 3, Appli	Sequence 3, Appli

## ALIGNMENTS

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FILING DAYE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/835,713
APPLICATION NUMBER: US/07/835,713
FILING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: CONLIN, David G.
REGISTRATION NUMBER: 27026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEX: 200291 STRE UR
TELEPAX: (617)523-6440
TELEX: 200291 STRE UR
TELEPAX: 143 base pairs
LENGTH: 1493 base pairs
TYPE: DUCLEIC acid
 . Sequence 24, Application US/08340820
 GENERAL INFORMATION:
 MOLECULE TYPE: CI
HYPOTHETICAL: NO
ANTI-SENSE: NO
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 APPLICANT: KONDO, Tatsuya
TITLE OF INVENTION: GLIA ACTIVATING
TITLE OF INVENTION: PRODUCTION
NUMBER OF SEQUENCES: 27
ORIGINAL SOURCE: ORGANISM: Hom
 CORRESPONDENCE ADDRESS:
 APPLICANT: NARUO, Ken-ichi
APPLICANT: SEKO, Chisako
APPLICANT: KUROKAWA, Tsutomu
 TYPE: nucleic acid
STRANDEDNESS: double
 APPLICATION NUMBER:
 STREET: 130 V
 ADDRESSEE: DAVID G. CONLIN;
ADDRESSEE: CUSHMAN
 Massachusetts
 130 Water Street
 linear
 CDNA to mRNA
 US/08/340,820
 DIKE,
 BRONSTEIN, ROBERTS
 FACTOR
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 RESULT 2
US-08-593-535-24/c
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 US-08-340-820-24
 Matches
 Query Match
 Patent No.
 GENERAL INFORMATION:
 TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO:
 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/593,535
FILING DATE: 24-JAN-1996
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0;
FILING DATE: 12-EBB-1992
ATTORNEY/AGENT INFORMATION:
 APPLICANT:
 1409
 MOLECULE TYPE:
HYPOTHETICAL:
 SEQUENCE CHARACTERISTICS:
LENGTH: 1493 base pairs
TYPE: nucleic acid
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 TITLE OF INVENTION: GLIA ACTIVATING FACTOR AND ITS TITLE OF INVENTION: PRODUCTION NUMBER OF SEQUENCES: 27 CORRESPONDENCE ADDRESS:
 TELEPHONE: (617)523-3400
 APPLICANT:
 1349 GAGGTCTTTGCTTT 1336
 LIBRARY: Human
 140
 HAPLOTYPE: 211
TISSUE TYPE: skin
Tissue Type: fibroblast
 NAME: CONLIN, David G. REGISTRATION NUMBER: 2
 80 TATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTAGTTCGGGTTTGAGAAA 139
 TOPOLOGY:
 STRANDEDNESS:
 CLASSIFICATION:
 COMPUTER:
 COUNTRY:
 ADDRESSEE:
 Local Similarity es 77; Conserv
 CLONE:
 5622928
 AGGGTTTCGACTTT 153
 Boston
 pGAF1
 Massachusetts
 Application US/08593535
 130 Water Street
 KONDO, Tatsuya
 Human foreskin cDNA library
 KUROKAWA, Tsutomu
 Conservative
ĕ
 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
 linear
 DAVID G. CONLIN;
 ĕ
 Floppy disk
 cDNA to mRNA
 double
 Chisako
 12.0%;
 Ken-ichi
 US 07/835,713
 27026
 24:
 0
 Score 42.8; DB Pred. No. 0.94;
 DIKE, BRONSTEIN, ROBERTS
 Mismatches
 DB 1;
 #1.25
 57;
 Length 1493;
 Indels
 0
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 ; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
US-09-122-400B-5
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 ; CLONE: p
US-08-593-535-24
 US-09-122-400B-5/c
 Matches
 Query Match
Best Local Similarity
 Sequence 5, Application US/09122400B Patent No. 6245974
 GENERAL INFORMATION:
 Matches
 Query Match
Best Local :
 FILE REFERENCE: Michalowski and Spiker CURRENT APPLICATION NUMBER: US/09/122,400B CURRENT FILING DATE: 1998-07-24
 APPLICANT: Spiker, Steven
TITLE OF INVENTION: MATRIX ATTACHMENT REGIONS
 APPLICANT: Michalowski, Susan APPLICANT: Spiker, Steven
 PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1997-08-06
 NUMBER OF SEQ ID NOS:
 1409
 1349 GAGGTCTTTGCTTT 1336
 ORIGINAL SOURCE:
ORGANISM: Homo sapiens
HAPLOTYPE: 2n
 CELL TYPE: fib
IMMEDIATE SOURCE:
LIBRARY: Human
439 TCAGCTTCTTTTTTTCAGTTTTTA 415
 185 TAGGTTGAGTCTTTGGACATTTGTA 209
 499
 125 TICGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGC 184
 619 AAAAAAGAAGAAATATTTTTTTTTTTAGTTTTTACAAAATATTGTTTTAGAAAATATT 560
 140
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 80
 Local
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 TTCAGTTTTTAGTAGTTTTTTCCAGATTTTACAAATAAAATTGCTTTAGAAAATTGATTT 440
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 . Similarity 57.9
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 Conservative
 Human foreskin cDNA library
 fibroblast
 skin
 153
 11.7%;
 12.0%;
 60/066,118
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 Score 42.8; DB Pred. No. 0.94; 0; Mismatches
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Pred. No. 1
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 BB
 DB 1;
 4.
 57;
 Length 998;
 Length 1493;
 Indels
 0
 0;
 Gaps
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US-08-378-313-24/c ; Sequence 24, Application US/08378313 ; Patent No. 6207881

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 ; LOCATION:
US-08-378-313-24
 Query Match
 Matches
 INFORMATION FOR SEQ ID NO:
 GENERAL INFORMATION:
APPLICANT: THEOLO
 2102
 2162
 FEATURE:
 SEQUENCE CHARACTERISTICS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 1922
 REFERENCE/DOCKET NUMBER: 29
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 856-5600
 PRIOR APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 1982
 2042
 ATTORNEY/AGENT INFORMATION:
 NUMBER OF SEQUENCES:
 IITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
 APPLICANT:
 184
 304
 244
 124
 64
 NAME/KEY:
 TOPOLOGY:
 TYPE: nucleic acid
STRANDEDNESS: sing
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
 TELEFAX:
 APPLICATION NUMBER: US 0 FILING DATE: 02-APR-1992
 CLASSIFICATION:
 FILING DATE:
 ADDRESSEE:
 REGISTRATION NUMBER:
 APPLICATION NUMBER:
 ENGTH:
 ocal
 TTTTTGCCCCAATGATATATAAAAATTTGGATAATAATATTATTGGATATTCGTTTTTTA 123
TTTGCATTCATTAATTAGCTAAGACAAATTATGATGTCTAAGTAC 1878
 TTAACATAACTTCACTTTTGCATTCATTAATTAGCTAAGACAAATTATGATGTCTAAGTA 2043
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 AAACCTTAAATGGGCTTTCTATAAGGCCCCAATTATATTACGATTATAACAAAGTGACAAC 303
 CTAGGTTGAGTCTTTGGACATTTGTATTGGATGTTGTTGATTAGTGTCGACACTATT 243
 155;
 94304-1018
 11.5%;
Similarity 44.9%;
 Palo Alto
 MURASHIGE, KATE
 California
 70614
 3: MORRISON & FOERSTER 755 Page Mill Road
 2230 base pairs
 (415) 494-0792
 USA
 Conservative
 SATO,
 THEOLOGIS, ATHANASIOS
 CDS
 91..1545
 linear
 single
 TAKAHIDO
 US 07/862,493
 US/08/378,313
 29,959
 0;
 29190-20002.20
 Score 41; DB of Pred. No. 2.1;
 Mismatches 190; Indels
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 0,
 Gaps
 0;
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 US-09-056-075-1/c
 US-09-056-075-1
 sequence 1, Application US/09056075
Patent No. 5955368
 Query Match
Best Local Similarity
 Matches 155;
 GENERAL INFORMATION:
 TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO:
 1356
 REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 1296
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 MOLECULE TYPE:
 SEQUENCE CHARACTERISTICS:
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 CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION:
 APPLICANT:
 APPLICANT:
 APPLICANT:
 NUMBER OF
 123 AGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGA 182
303
 243 TAAACCTTAAATGGGCTTTCTATAAGGCCCAATTATATTACGATTATAACAAAGTGACAA 302
 64
 OTHER INFORMATION: /note- "RP4 origin of DNA transfer (oriT) from OTHER INFORMATION: plasmid RP4"
 NAME/KEY: misc_feature LOCATION: 3770..4013
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
 STREET:
 TOPOLOGY:
 STRANDEDNESS:
 REGISTRATION NUMBER:
 FILING DATE:
 SOFTWARE:
 COUNTRY:
 ADDRESSEE:
 TELEPHONE:
 APPLICATION NUMBER:
 ENGTH:
 TTTTTGCCCAATGATATAAAAAATTTGGATA-AATAATATTATTGGATATTCGTTTTTT 122
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 Madison
 53701-2113
 nucleic acid
 Seay, Nicholas
 Σï
 SEQUENCES:
 6243 base pairs
 E: Quarles & Brady
1 South Pinckney S
 SD
 Johnson, Eric A.
Bradshaw, Marite
 Conservative
 PatentIn Release #1.0,
 608-251-5000
 DNA (genomic)
 double
 Julian
 11.4%;
47.3%;
 Expression System for Clostridium Species
 US/09/056,075
 27386
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 Street
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Pred. No. 2
 Mismatches
 Version #1.30
 DВ
 172;
 2:
 Length 6243;
 Indels
 1;
 Gaps
 1177
 1237
 1297
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 PCT-US92-06300-1
 PCT-US92-06300-1/c Sequence 1, Application PC/TUS9206300
 Matches
 Query Match
 GENERAL INFORMATION:
 TELEFAX: (215) 962-4107 INFORMATION FOR SEQ ID NO:
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
FILING DATE: 19920730
 SEQUENCE CHARACTERISTICS:
 TELEPHONE: (215) 962-4130
 ATTORNEY/AGENT INFORMATION:
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 MOLECULE TYPE:
 CORRESPONDENCE ADDRESS:
 APPLICANT: Nathan, Margret
APPLICANT: Shani, Moshe
TITLE OF INVENTION: Transgenic Protein Production
NUMBER OF SEQUENCES: 1
 PUBLICATION INFORMATION:
 ANTI-SENSE:
 IYPOTHETICAL:
 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polocial
 62
 NAME: Goodman, Rosanne REGISTRATION NUMBER: 52, REFERENCE/DOCKET NUMBER:
 Local Similarity
 RELEVANT RESIDUES IN SEQ ID
 AUTHORS:
 AUTHORS:
 AUTHORS:
 AUTHORS:
 AUTHORS:
 TOPOLOGY:
 STRANDEDNESS:
 CLASSIFICATION:
 COUNTRY:
 STREET:
 LENGTH:
 ADDRESSEE:
TTTTTTTGCCCAATGATATAAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTT 121
 1986
 19034
 NUCLEIC ACID
 Ft. Washington
 S: Kuang, W.-J.
S: Dennison, O E
S: Hawkins, J W
S: Beattle, W G
S: Beattle, W G
S: Dugaiczyk, A
MOLECULAR STRUCTURE OF THE HUMAN ALBUMIN GENE
IS REVEALED BY NUCLEOTIDE SEQUENCE WITHIN Q11-22
OF CHROMOSOME 4
 6747-6757
 Pennsylvania
 J. Biol.
261
 500 Virginia Ave.,
 Minghetti, P P
Ruffner, D E
 USA
 Conservative
 PatentIn Release #1.0, Version #1.25
 Hurwitz, David R
 linear
 ĕ
 Rhone-Poulenc Rorer, Inc. 0 Virginia Ave., Bldg. 3A
 ŏ
 19920730
 DNA (genomic)
 double
 11.4%; 52.3%;
 Chem.
 PCT/US92/06300
 52,534
 0;
 A0856-US
 Score 40.8; D
Pred. No. 2.3;
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 Mismatches
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 FROM 1 TO 19002
 DB 5;
 82;
 Length 19557;
 Indels
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 US-09-073-569-1
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 us-09-073-569-1/c
 Matches
 Query Match
Best Local S
 Sequence 1, Application US/09073569 Patent No. 6084088 GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1733 base pairs
 1715
 FILING UNITED ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A
REGISTRATION NUMBER: 37,438
REGISTRATION NUMBER: 97-14
1595
 1655
 CURRENT APPLICATION DATA
 COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
 FEATURE:
 TELEPHONE: 206-442-6672
 PRIOR APPLICATION DATA: APPLICATION NUMBER:
 140
 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION:
 APPLICANT: Grossmann,
 NAME/KEY:
 122 TAGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATAT 173
 80
 OPERATING SYSTEM:
SOFTWARE: FastSEC
 OTHER INFORMATION:
 TOPOLOGY:
 STRANDEDNESS:
 TYPE:
 TELEFAX: 206-442-6678
 CLASSIFICATION:
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 COUNTRY:
 STREET:
 ADDRESSEE:
 AGGGTTTCGACTTTC 154
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 AGGGTCTGTATTATC 1581
 Similarity
 nucleic acid
 98102
 Seattle
 WA
 E: ZymoGenetics, Inc.
1201 Eastlake Avenue East
 USA
 Conservative
 SYSTEM: DOS
FastSEQ for Windows Version
 Coding Sequence 34...1344
 linear
 IBM Compatible
 Diskette
 single
 NOVEL TUMOR ANTIGENS
 11.3%;
 us/09/073,569
 Angelika
 0,:
 Score 40.6;
Pred. No. 2.
 Mismatches
 DB
 59;
 <u>ω</u>
 Length 1733;
 Indels
 <u>.</u>
 Gaps
 0
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 US-08-078-090-3
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 5231168-1
 PATENT NO. 5231168

APPLICANT: DZIBGIEL, MORTEN; BORRE, MARTIN; JEPSEN, SOREN; VUUST, JENS; RIENECK, KLAUS; WIND, ANNETTE; JAKOBSEN, PALLE H. TITLE OF INVENTION: MALARIA ANTIGEN NUMBER OF SEQUENCES: 19

CURRENT APPLICATION DATA:
 5231168-1; Patent No.
 Sequence 3, Patent No.
 SEQ ID NO:]
 Matches
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SEQUENCE CHARACTERISTICS:
 REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: BE
TELECOMMUNICATION INFORMATION:
 ATTORNEY/AGENT INFORMATION:
 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: WO POSITION DATE: 19-AUG-1992
 CURRENT APPLICATION DATA
 2724
 CORRESPONDENCE ADDRESS:
 APPLICANT: STROEMQUIST, MATS
TITLE OF INVENTION: HUMAN BETA-CASEIN PROCESS FOR PRODUCING
TITLE OF INVENTION: IT AND USE THEREOF
 2784 TTATATATAAATACTGGATAAATATTTATGTATATATTTATAT 2826
 NUMBER OF SEQUENCES:
 APPLICANT:
 APPLICANT:
 PPLICANT:
 NAME: COOPER, IVER P. REGISTRATION NUMBER: :
 APPLICATION NUMBER: FILING DATE: 19-AUC
 APPLICATION NUMBER: U. FILING DATE: 19930618
 CLASSIFICATION:
 SOFTWARE:
 OPERATING SYSTEM:
 MEDIUM TYPE:
 COUNTRY:
 STREET:
 64
 ADDRESSEE:
 Local Similarity
 FILING DATE: 18-SEP-1989
 APPLICATION NUMBER:
 LENGTH: 3095
 TTTTTGCCCAATGATATATAAAATTTGGATAAATAATATTAT 106
 INFORMATION:
 64;
 20004
 WASHINGTON
 READABLE FORM:
 D.C
 Application US/08078090
 419 SEVENTH STREET, N.W.
 (202)628-5197
(202)737-3528
 USA
 HERNELL, OLLE
LOENNERDAL, BO
HJALMARSSON, KAI
 PatentIn Release #1.0, Version #1.25
 TOERNELL,
 HANSSON, LENNART
 BERGSTROEM, SVEN
 Conservative
 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
 BROWDY AND NEIMARK
 IUMBER: WO PCT/DK91/00233
19-AUG-1991
 Floppy disk
 11.3%;
 WO PCT/DK92/00236
 JAN
 US/08/078,090
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 US/07/409,658
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 KARIN
 BERGSTROM2
 Score 40.6; DB Pred. No. 2.5; 0; Mismatches
 0,
 DB
 39;
 6;
 Length 3095;
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 Gaps
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RESULT 10
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 US-08-078-090-3
 Query Match
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 Matches
 Patent No. 6096950
 Matches
 Query Match
 INFORMATION FOR SEQ ID NO:
 ATTORNEY/AGENT INFORMATION:
NAME: Baker, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 670
 SEQUENCE CHARACTERISTICS:
 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 MOLECULE TYPE:
 TELEPHONE: (414) 277-5709
 CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION:
 NUMBER OF SEQUENCES:
 1043 GTAGATTAGT 1052
 TYPE: nucleic acid
STRANDEDNESS: double
 FEATURE:
 STRANDEDNESS:
TOPOLOGY: lir
 MOLECULE TYPE:
 180 GGAGCTAGGT 189
 120 TTTAGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTG 179
 923 ATTTATAGTATAGAAATGAGTATAAAAACTAGTATAATTAGTATTAGTATATATTAGTAT 982
 FILING DATE:
CLASSIFICATION: 800
 APPLICATION NUMBER:
 CITY: Milwaukee
 60 ATTITTTTTGCCCAATGATATATAAAAATTTGGATAAATAATATTATTGGATATTCGTTT 119
 COUNTRY:
 ADDRESSEE:
 Local Similarity les 74; Conserv
 LOCATION:
 LOCATION:
 NAME/KEY:
 TOPOLOGY:
 STRANDEDNESS:
 LENGTH:
 INFORMATION:
 'RY: U.S.A.
53202-4497
 Application US/08749522
 : 10607 base pairs
 : (414) 277-57
(414) 271-3552
 411 East Wisconsin Avenue
 Conservative
 linear
 Conservative
 join(4804..4854, 5720..5746, 6726..6746, 6845
..6886, 7991..8521, 9440..9445)
 Quarles
 linear
 DNA (genomic)
 DNA (genomic)
 single
 Maliyakal
 11.2%;
 277-5709
 11.3%; 56.9%;
 FIBER-SPECIFIC PROMOTERS
 & Brady
 US/08/749,522
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 670513.90244
 Score 40; DB 3; Le
Pred. No. 3.3;
0; Mismatches 180;
 Score 40.4; D
Pred. No. 2.8;
 Mismatches
 DB 1;
 Length 2755
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 RESULT 11
US-08-341-568-3/c
 Sequence 3, Application US/08341568
Patent No. 5661021
GENERAL INFORMATION:
 ATJORNEY/AGENT INFORMATION:
NAME: MUTPHY JI, Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 365-262P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPHONE: (703) 205-8050
 TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 APPLICANT:
 SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/341,568
FILING DATE: 22-NOV-1994
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 APPLICANT: Saloheimo, Anu APPLICANT: Marjatta, Ranua TITLE OF INVENTION: Methods TITLE OF INVENTION: pulps
 MOLECULE TYPE: ORIGINAL SOURCE:
 2046 ATATAACTAGTAATGTATTTTGACTTTTTTTAATCGAGTTAATGTTGGTTATTTCG
 NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
 2166 TGAAGTAAAATTATTTAACAAATATATTTTGAAAAATTGATAAAAATACTAAATGAGGTT 2225
 APPLICANT:
 66
 STREET: PO Box 747
CITY: Falls Church
 LENGTH: 289 base pairs
TYPE: nucleic acid
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
 COUNTRY: US
ZIP: 22040-0747
ORGANISM:
 TOPOLOGY:
 STRANDEDNESS:
 CLASSIFICATION:
 ADDRESSEE:
 TAGGTTGAGTCTTTGGACATTTGTATTGGATGTTGTTGATTATTAGTGTCGACACTATTA 244
 TTATACCAATTCAATAAAATATTTTATTTATATTAAATTATAGCATACTCACGATGTGGG
 TTAGTTTATGGTTGATTGATCGATAATACCAAATTTATTAAAAATTAATATTAG 2397
 TTTACTTCGTTTTTGATCCGAAGCAATAACAAATTGTCAAATACCAAACACAAG 358
 AACCTTAAATGGGCTTTCTATAAGGCCCAATTATATTACGATTATAACAAAGTGACAACT 304
 TCGGGTTTGAGAAAAGGGTTTCGA-CTTTCGAAAGTGGACGATGTATATAGATTGGGAGC
 TTTGCCCAATGATATAAAAAATTTGGATAAATAATAATATTGTATTGGATATTCGTTTTTTAGT 125
 ATGTGTATATTTG--TACTATTATTCTATATAAATTGATAACCTTATAAAAGTATCTAAT 2343
 TTGGTTGAATAGTAAGATATAATTATTACAAATTATAAAATATGTAGGTTCAAAATCTATC
 ٧A
 Viikari, Liisa
Penttila, Merja
 Siika-aho,
 PatentIn Release #1.0, Version #1.30
 Trichoderma reesei
 linear
 Birch, Stewart, Kolasch and Birch
 CDNA
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 Johanna
 Mannanase enzymes, genes coding for them, methods for isolating the genes, and methods for bleaching lie
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 2285
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 RESULT 12
 US-08-341-568-3
 Sequence 3,
 Query Match
Best Local :
 Patent No.
 Matches
 TELEX: 248345
INFORMATION FOR SEQ ID NO:
 GENERAL INFORMATION:
 MOLECULE TYPE: cDN
ORIGINAL SOURCE:
ORGANISM: Trichc
STRAIN: QM9414
 APPLICANT:
 REFERENCE/DOCKET NUMBER: 36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
 SEQUENCE CHARACTERISTICS:
LENGTH: 289 base pairs
 APPLICATION NUMBER: US 0
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
 APPLICATION NUMBER: (FILING DATE: 13-AUG-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
 APPLICANT: Saloheimo, Anu
APPLICANT: Marjatta, Ranua
TITLE OF INVENTION: Mannanase enzymes, genes coding for them,
TITLE OF INVENTION: methods for isolating the genes, and meth
TITLE OF INVENTION: lignocellulosic pulps
NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 APPLICANT:
 217 TATATATATATTCATCAAAAA 197
 TOPOLOGY:
 STRANDEDNESS:
 TELEFAX:
 NAME: Murphy Jr, Gerald M
REGISTRATION NUMBER: 28,977
 STREET:
 80 TATAAAAATTTGGATAAATAA 100
 COUNTRY:
 ADDRESSEE:
 Local
 Falls Church
 nucleic acid
 22040-0747
 Similarity
 ٧A
 Application US/08911020
 PO Box 747
 (703) 205-8050
 S
 Siika-aho, Matti
Viikari, Liisa
Penttila, Merja
 Buchert,
 Conservative
 linear
 Trichoderma reesei
 13-AUG-1997
 single
 11.0%;
67.9%;
11.0%;
 Johanna
 Stewart, Kolasch and Birch
 US 08/341,568
 US/08/911,020
 <u>ω</u>
 365-262P
Score 39.4; D
Pred. No. 4.3;
 Score 39.4; DB 1; Pred. No. 4.3;
 Mismatches
 26;
 Length 289;
 Length 289;
 Indels
 and methods for bleaching
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Matches

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Mismatches

Indels

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Best Local Similarity

Query Match

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; MOLECULE TYPE:
; HYPOTHETICAL: N
; ANTI-SENSE: NO
US-08-487-826B-13
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 RESULT 13
US-08-487-826B-13/c
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 Query Match
Best Local Similarity
 15695
 TELEFAX: (619) 235-017
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pai:
 126 TCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATA---GATTGGGA 182
 REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
 STREET: 620 NC., CITY: Newport Beach STATE: California
 ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 tent No.
 APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
 66 TTTGCCCAATGATAATAAAAATTTGGATAAATAATAATATTGGATATTCGTTTTTTAGT 125
 NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS
 TITLE OF INVENTION:
 APPLICANT:
 APPLICANT:
 TOPOLOGY:
 STRANDEDNESS:
 APPLICATION NUMBER: US/0
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
 TELEPHONE:
 NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
 217 TATATATATTCATCAAAAA 197
 277
 ADDRESSEE:
20
 161;
 TATAAAATTTGGATAAATAA 100
 INFORMATION:
 13, Application US/08487826B
5. 5993827
 H: 19124 base pairs nucleic acid
 E: Knobbe Martens Olson & Bear
620 Newport Center Drive 16th Floor
 Conservative
 ĕ
 Wellems,
 linear
 Su, Xin-zhaun
 Peterson, David S
 (619) 235-8550
(19) 235-0176
 CDNA
 single
 11.0%;
 BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
 Thomas E.
 US/08/487,826B
 13:
 Score 39.4; D
Pred. No. 4.4;
0; Mismatches
 0;
 NIH121.001CP1
 DB 2;
 181;
 Length 19124;
 Indels
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 Gaps
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Ahes 75; Conserve
 ; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
;US-09-410-464-1
 RESULT 15
US-09-410-464-1
 밁
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 ; LENGTH: 1895
; TYPE: DNA
; ORGANISM: Brachydanio rerio (zebra fish)
US-09-444-336-7
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 SOFTWARE:
SEQ ID NO 1
 US-09-444-336-7/c
 밁
 Sequence 1, Application US/09410464 Patent No. 6395892 GENERAL INFORMATION:
 Q
 CURRENT APPLICATION NUMBER: US/09/410,464
CURRENT FILING DATE: 1999-10-01
EARLIER APPLICATION NUMBER: 09/287,700
EARLIER FILING DATE: 1999-04-06
EARLIER APPLICATION NUMBER: 60/080,851
EARLIER FILING DATE: 1998-04-06
NUMBER OF SEQ ID NOS: 24
 Query Match
Best Local Similarity
 APPLICANT: Strauss et al.
TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
FITLE OF INVENTION: poplar and other plant species.
FILE REFERENCE: 53375
 Matches
 SEQ ID NO 7
 Sequence 7, Application US/09444336 Patent No. 6410713 GENERAL INFORMATION:
 APPLICANT: Guerriero, Vincent APPLICANT: Raynes, Deborah A TITLE OF INVENTION: DNA Encoding Proteins That Inhibit Hsp70 Function FILE REFERENCE: HspBr DNA and Protein Sequences CURRENT APPLICATION NUMBER: US/09/444,336 CURRENT FILING DATE: 1999-11-19 EARLIER APPLICATION NUMBER: 60/109,351 EARLIER APPLICATION NUMBER: 60/109,351 EARLIER FILING DATE: 1998-11-20
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 SOFTWARE: PatentIn Ver.
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 1802 GGTCTGAATGTGTTTAATTTTAATTATTGTCTATT 1768
 80 TATAAAAATTTGGATAAATAATATTATTGGATATT 114
 303 CITTTACTTCGTTTTGATCCGAAGCAATAACAAATTGTCAAATA 347
 243 TAAACCTTAAATGGGCTTTCTATAAGGCCCCAATTATATTACGATTATAACAAAGTGACAA 302
 183
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 PatentIn
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63.2%;
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5.2;
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 0;
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 242
 15576
 0;
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Gaps

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Maximum DB
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Maximum Match 100%
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Perfect score:
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358
 March 30,
 Published_Applications_NA:*
 GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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9 US-10-176-918-345
9 US-10-137-665-345
9 US-10-140-474-345
 DВ
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 US-09-960-352-5785
US-10-102-806-401
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 SUMMARIES
Sequence 5785, Apsequence 401, App Sequence 12673, A Sequence 26, Appl Sequence 360, Appl Sequence 340, App Sequence 3759, App Sequence 3759, App Sequence 345, App
 1148742
 Description
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 RESULT 1
US-09-960-352-5785
; Sequence 5785, A
 GENERAL INFORMATION:
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US-09-960-352-1243	US-09-885-303A-11	- S	05-09-813-183-3E	IIS-09-816-894-5	US-09-960-353-170	3-1	IIS-10-013-477-0	TS-09-935-303-3	7	IIS=10=374-000-3	200	TS-00-870-874 12622	12-19-938-819-120C	2.0	50	5	TIS-09-990-107 3302	֓֞֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓	TS-10-141-755-345	<u> </u>	TS-10-143-433-345	TS-10-133-363-345	TS-10-140-002-345	ַה הַ	- 2 - 1
9-9	7 8 8	0	81	ָה מים	9	200	5	200	,	ָ טְּ	200	2	0	2	9-7	9-7		2 6	2 5	2 6	) i	2 i	2 0	10-140-000	2
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352	750	יו מיני	5 U	0 0	л C	2 7	10		200	5 0	0 0	1 1	֓֞֝֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓	3 (	7 0	л F	1 0	ָט נ ט נ	100	200	707	7 7	200	14	
-12	֓֞֜֜֜֝֜֜֜֝֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֡֜֝֓֓֓֓֓֡֜֝֓֡֓֡֓֡֓֜֝֡֓֡֓֡֡֝֡֡֡֓֡֓֡֡֡֜֝֡֡֡֡֜֝֡֡֡֡֡֡֡֡		ט מ	4	1 0	1	֓֞֞֜֜֞֜֞֜֞֜֜֜֓֓֓֓֞֜֜֜֓֓֓֓֓֞֜֜֓֓֓֓֡֝֓֓֜֝֓֡֝֝֓֡֝֝֡֝֝֝֡֝֝֡֝֝֡֝֝֡ ֖֖֖֖֓	ט נ	٠,	֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓֓		4 4	-		0 1	ر د	10	4	2	4		2 4		1440	,
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Sequence 11, Appl Sequence 1243, A	an Pe	Juer	nbe	aqu.	equ	quei	equ	equ	que	equ	egu	Sequence 4296, Ap	equ	que	Sequence 2, Appli	equ	equ	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	
ence	nce	e	ence	ence	ence	псе	enc	enc	nce	enc	enc	nce	enc	nce	nce	enc	enc	nce	nce	nce	nce	nce	nce	nce	
11,	4.5	35,	5	17	e 7	Ņ	e w	w	'n	e G	e 1	42	e 1	ω	Ņ	œω	e 2	ω A	34	34	34	34	345	ω 4	
A A F	84,	ě	`	707	, 90	Ą	15,	` ≥.	Ą	558	397	96,	241	Ą	Αp	327	0	5	,	Ç	Ġ	Ü	٦,	Ġ	
equence 11, Appl Sequence 1243, Ap	Sequence 4584, Ap	Sequence 35, Appl	ğ	Sequence 1707, Ap	Αþ	Sequence 2, Appli	A	Sequence 3, Appli	Ĕ.	Sequence 5558, Ap	Sequence 13973, A	ð	Sequence 12412, A	p1 1	P11	Σ,	Sequence 20, Appl	aga:	gg.	aga,	App	App	aga.	Αpp	
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## ALIGNMENTS

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RESULT 2
US-10-102-806-401/c
; Sequence 401, Application US/10102806
 APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/99/960,352
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 5785
LENGTH: 516
 Query Match 13.4%;
Best Local Similarity 65.4%;
Matches 70; Conservative
 sequence 5785, Application US/09960352
Patent No. US20020137139A1
 FEATURE:
NAME/KEY: unsure
LOCATION: (76), (90)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: 25-LIB3057-018-Q1-K1-G1
 TYPE: DNA
ORGANISM: Bos taurus
 80 TATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTAGTT 126
 0; Mismatches
 Score 47.8; DB 10; Length 516; Pred. No. 0.78;
 37;
 0,
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 0;
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Publication No.

US20030054421A1

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 RESULT 3
US-09-960-352-12673/c
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 US-10-102-806-401
 CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
 SEQ ID NO 12673
LENGTH: 277
 GENERAL INFORMATION:
 Sequence 12673, Application US/09960352 Patent No. US20020137139A1
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 NUMBER OF SEQ ID NOS: 846
SOFTWARE: Patentin Ver. 2
SEQ ID NO 401
LENGTH: 189
TYPE: DNA
 APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Negappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TILE REFERENCE: 15511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
 APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103PLC1
 GENERAL INFORMATION:
 APPLICANT: Warren, Wesley C.
ORGANISM: Bos taurus
ORGANISM: DOS taurus
COMPUTED THEORMATION: Clone ID:
 TYPE: DNA
 OTHER INFORMATION: n equals a,t,g, or
 LOCATION: (162)
OTHER INFORMATION: n equals
NAME/KEY: misc_feature
 LOCATION: (166)
OTHER INFORMATION: n equals a,t,g,
 NAME/KEY: misc_feature
LOCATION: (187)
 NAME/KEY: misc_feature
LOCATION: (162)
 NAME/KEY: misc_feature LOCATION: (1)
 ORGANISM: Homo sapiens FEATURE:
 NAME/KEY: misc_feature LOCATION: (166)
 OTHER INFORMATION: n equals
 LOCATION: (11)
OTHER INFORMATION: n equals
 NAME/KEY: misc_feature
 OTHER INFORMATION: n equals a,t,g,
 80
 98 TATTAAAATAAACATGTATAGCAGGTTTCAACAATTGTCTTGTAGTTTG 50
 TATAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTAGTTCG 128
 Similarity
 Conservative
 12.6%;
 2.0
 a,t,g,
 a,t,g,
 a,t,g,
 54-LIB3058-039-Q1-K1-F10
 Score 45; DB 9
Pred. No. 2.1;
0; Mismatches
 0;
 or.
 압
 압
 DB 9; Length 189
 40;
 Indels
 0
 Gaps
 0;
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 SOFTWARE: Patentin Ver. 2
SEQ ID NO 26
LENGTH: 681
TYPE: DNA
ORGANISM: Homo sapiens
 US-09-960-352-5094
 RESULT 5
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 US-09-822-830A-26
 US-09-822-830A-26
 RESULT 4
 US-09-960-352-12673
 Sequence 5094, Application US/09960352 Patent No. US20020137139A1 GENERAL INFORMATION:
 Query Match
Best Local Similarity
Matches 80; Conserv
 Matches
 GENERAL INFORMATION:
 Sequence
 Best Local
 Query Match
 Patent No.
APPLICANT: Warren, Wesley C. APPLICANT: Tao, Nengbing
 PRIOR APPLICATION NUMBER: 60/195,604
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEC. TO
 CURRENT APPLICATION NUMBER: US/09/822,830A CURRENT FILING DATE: 2001-03-29
 FILE REFERENCE: GIN 6402
 APPLICANT: Graham, James R.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
 APPLICANT:
 APPLICANT:
 APPLICANT:
 APPLICANT: Genetics Institute, Inc
 APPLICANT:
 APPLICANT:
 441
 140
 381
 321
 155 TTTTTTTTTTTAAAAAAA 137
 122 TAGTTCGGGTTTGAGAAAA 140
 80
 62 TTTTTTTGCCCAATGATATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTT 121
 ATAAGCTTTATTACATCAAGTAATAAATACATACAAAGATGCAAACAGTTTTAGTCATT
 AGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTAGGTTGAGTCTTT 198
 TATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTAGTTCGGGTTTGAGAAA 139
 26, Application US/09822830A
5. US20020142952A1
 95;
 Similarity
 Gulukota, Kamalakar
 Howes, Steven H.
Resnick, Richard J.
 Agostino, Michael J.
 Fechtel, Kim
 Clark, Hilary
 Wong, Gordon
 Conservative
 Conservative
 12.5%;
 12.5%;
53.1%;
 0;
 0;
 Score 44.6; Di Pred. No. 3.6;
 Score 44.6; D
Pred. No. 2.8;
 Mismatches
 Mismatches
 DB
 DB 10;
 10;
 59;
 84;
 Indels
 Length
 Indels
 Length
 0;
 0;
 Gaps
 Gaps
 156
 0
 0;
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APPLICANT:

Byatt, Māthialagan,

John C

Nagappan

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION FILE REFERENCE: 16511.006/37-21(10298)C

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 ; LENGTH: 446
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 15-LIB3058-052-Q1-K1-D11
US-09-960-352-3400
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 δã
 US-09-960-352-3400
 В
 Q
 ; NAME/KEY: unsure
; LOCATION: (17),(37),(41)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 22-LIB3058-042-Q1-K1-F9
US-09-960-352-5094
 Query Match
Best Local Similarity
 Matches 114;
 APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 16511,006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
 GENERAL INFORMATION:
 Sequence 3400, Application US/09960352 Patent No. US20020137139A1
 Matches
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 NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 5094
 200 GACATTTGTATTGGATGTTGTTGATTATTAGTGTCGACACTATTAAACCTT 250
 CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
 203
 143
 LENGTH: 277
TYPE: DNA
ORGANISM: Bos taurus
FEATURE:
 80 TATAAAAATTTGGATAAATAATAATTATTGGATATTCGTTTTTTAGTTCGGGTTTGAGAAA 139
 263
 Local 5.
 AGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTAGGTTGAGTCTTTG 199
 TTATTTTTTTTTTA 277
 TTAGTTCGGGTTTGA 135
 Similarity 57.8
78; Conservative
 Conservative
 12.2%;
 12.2%;
 0; Mismatches
 Score 43.8; D
Pred. No. 4.6;
 Score 43.8;
Pred. No. 4;
 Mismatches
 DB 10;
 117; Indels
 DB 10;
 57;
 Length 446;
 Indels
 Length 277;
 0;
 <u>.</u>
 Gaps
 Gaps
 262
 0
 0
 US-09-960-352-2919

Sequence 2919, Application US/09960352

Patent No. US20020137139A1
 В
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 RESULT 8
 ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-444-759
 NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 2919
 GENERAL INFORMATION:
 RESULT 7
US-09-770-444-759
 Query Match
Best Local (
 Matches
 SOFTWARE: FastSEQ for Windows Version SEQ ID NO 759
LENGTH: 413
 CURRENT APPLICATION NUMBER: US/09/770,444
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,502
PRIOR FILING DATE: 2000-01-27
 Patent No.
 NUMBER OF SEQ ID NOS: 999
 APPLICANT:
APPLICANT:
APPLICANT:
 LENGTH: 447
 PPLICANT:
 APPLICANT:
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 PPLICANT:
 APPLICANT:
 APPLICANT:
 80 TATAAAATTTGGATAAAT 98
 82
 Local
 TCCAGAACTTTTTATAAAT 100
 l Similarity
57; Conserv
 US20020023280AJ
 An, Yong-Qiang
Hamilton, Carol M
Price, Jennifer L
Raines, Tracy M.
 Gorlach, Jorn
 Hoffman, Neil
 Davis, Keith R. Allen, Keith
 Ledford, Brooke L.
Woessner, Jeffrey P.
Haas, William David
 Garcia, Carlos A.
 Yu, Yang
Rameaka, Joshua G.
 Matthew, Abraham V.
 Conservative
 Page, Amy
 Application US/09770444
 (PARA-016PRV)
 72.2%;
 Score 43.8;
Pred. No. 4.
 Mismatches
 DB 10;
 22;
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373
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
 APPLICANT: Hurban, patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2027 (PARA-016PRV)
 22 Tranining transfer of the second s
 Length 447;
 Indels
 0;
 Gaps
 0;
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RESULT 10
US-10-028-072-345/c
; Sequence 345, Appli
; Publication No. US2
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 ; LENGTH: 414
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone
US-09-960-352-6528
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 US-09-960-352-6528
 US-09-960-352-2919
 Sequence 6528, Application Patent No. US20020137139A1 GENERAL INFORMATION:
 Best Loc
Matches
 Query Match
Best Local Similarity
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 SEQ ID NO 6528
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 APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathalagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES.
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 15511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
 TYPE: DNA
ORGANISM: Bos tauri
OTHER INFORMATION:
 142
 322
 140
 200
 262
 202
 267
 183
 207
 147
 123
 80
 20
 63
 87
 Local Similarity
 w
 GACATTTGTATTGGATGTTGTTGATTATTAGTGTCGACACTATT 243
 TATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTAGTTCGGGTTTGAGAAA 139
 GCTAGGTTGAGTCTTTGGACATTTTGTATTGGATGTTGTTTGATTATT 228
 AGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTAGGTTGAGTCTTTG
 AGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGA
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 Bos taurus
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 Application US/10028072
o. US20030004311A1
 Conservative
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 12.2%;
 12.1%;
49.6%;
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 US/09960352
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 28-LIB3058-032-Q1-K1-G11
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 Score 43.2; DB 10;
Pred. No. 5.8;
0; Mismatches 113;
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 DB 10;
 114;
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 Length
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 ASSOCIATED WITH LACTATION AND
 413;
 0;
 0;
 Gaps
 Gaps
 261
 201
 182
 146
 206
 . ;
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 GENERAL INFO
APPLICANT:
APPLICANT:
 PRIOR
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 CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
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 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1997-00
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 PRIOR FILING DATE:
 PRIOR APPLICATION NUMBER: 60/056974
 TITLE OF INVENTION:
 APPLICANT:
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 APPLICATION NUMBER: 60/063733
 APPLICATION NUMBER: 60/063561
FILING DATE: 1997-10-28
APPLICATION NUMBER: 60/063704
FILING DATE: 1997-10-29
 APPLICATION NUMBER: 60/063550 FILING DATE: 1997-10-28
 FILING DATE: 1997-10-27
 APPLICATION NUMBER: 60/063045
 FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/062816
 APPLICATION NUMBER: 60/
FILING DATE: 1997-10-24
 FILING DATE: 1997-09-
FILING DATE:
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 APPLICATION NUMBER: 60/063327 FILING DATE: 1997-10-27
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 FILING DATE: 1997-10-24
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FILING DATE: 1997-10-17
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 APPLICATION NUMBER: 60/059836 FILING DATE: 1997-09-24
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 APPLICATION NUMBER: 60/059122
FILING DATE: 1997-09-17
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FILING DATE: 1997-09-17
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 APPLICATION NUMBER: 60/059588
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 APPLICATION NUMBER: 60/059352
 FILING DATE:
 APPLICATION NUMBER:
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 INFORMATION:
 Baker, Kevin
 Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
 Tumas, Daniel
Watanabe, Colin
 Gao, Wei-Qlang
 Wood, William
 Stewart, Timothy A
 Goddard, Audrey
 Gerritsen, Mary E.
 Filvaroff, Ellen
 Desnoyers,Luc
 DeForge, Laura
 Beresini, Maureen
 1997-10-17
 1997-08-26
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 1997-09-18
 1997-09-17
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 60/063127
 60/049911
 60/062814
 60/059263
 60/059117
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OR APPLICATION NUMBER: 60/081818
OR FILING DATE: 1998-04-15
OR APPLICATION NUMBER: 60/08299
OR FILING DATE: 1998-04-20
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OR FILING DATE: 1998-04-28
OR APPLICATION NUMBER: 60/08345
OR FILING DATE: 1998-04-29
OR FILING DATE: 1998-04-29
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/084607
OR APPLICATION NUMBER: 60/084627
OR APPLICATION NUMBER: 60/084627
OR APPLICATION NUMBER: 60/084627
OR APPLICATION NUMBER: 60/084627
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FILING DATE: 1998-04-14
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FILING DATE: 1997-11-24
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FILING DATE: 1997-11-21
APPLICATION NUMBER: 60/066453
FILING DATE: 1997-11-24
ADDITION OF THE PROPERTY OF THE PR
 APPLICATION NUMBER: 60/064809
FILING DATE: 1997-11-07
APPLICATION NUMBER: 60/065186
FILING DATE: 1997-11-12
 APPLICATION NUMBER: 60/064248
FILING DATE: 1997-11-03
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NUMBER: 60/085149
1998-05-12
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1998-05-07
 1998-03-31
 1997-12-1
 1998-01-23
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 60/081203
 60/079663
 60/079294
 60/074086
 60/073612
 60/072320
 60/069334
 60/063755
 60/063738
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 Query Match
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Matches 66
 PRIOR
 PRIOR
 2925
 JR APPLICATION NUMBER: 60/088026
JR FILING DATE: 1998-06-04
JR APPLICATION NUMBER: 60/088730
JR FILING DATE: 1998-06-10
JR APPLICATION NUMBER: 60/088741
JR FILING DATE: 1998-06-10
 APPLICATION NUMBER: 60/
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/
FILING DATE: 1998-07-07
 JR FILING DATE: 1998-05-15
NR APPLICATION NUMBER: 60/01
NR FILING DATE: 1998-05-22
JR APPLICATION NUMBER: 60/01
NR FILING DATE: 1998-05-22
NR FILING DATE: 1998-05-22
 APPLICATION NUMBER: 60/
FILING DATE: 1998-07-01
FILING DATE: 1998-0
APPLICATION NUMBER:
 IR APPLICATION NUMBER: 60/08
IR FILLING DATE: 1998-05-13
IR APPLICATION NUMBER: 60/08
IR FILLING DATE: 1998-05-13
IR APPLICATION NUMBER: 60/08
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 Indels
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Sequence 345, Application US/10121049
Publication No. US20030022239A1
GENERAL INFORMATION: APPLICANT: Baker, Kevin p. APPLICANT: Beresini, Maur Beresini, Maureen

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2865

80 TATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTA 123

0;

Gaps

0;

APPLICANT:

Deforge, Laura Desnoyers, Luc Filvaroff, Ellen Gao, Wei-Qiang

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; SEQ ID NO 345
; LENCTH: 2933
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-121-049-345
 RESULT 12
US-10-123-904-345/c
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 Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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LENGTH: 2933
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TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C54
 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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 APPLICANT:
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 TATAAAAATTTTGGATAAATAATATTATTGGATATTCGTTTTTTA 123
 66;
 Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
 Wood, William
 Tumas, Daniel
 Gao, Wei-Qiang
 Filvaroff, Ellen
 Watanabe, Colin K
 Stewart, Timothy A.
 Smith, Victoria
 DeForge, Laura
 Tumas, Daniel
Watanabe, Colin K
Wood, William
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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 Conservative
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 Indels
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US-10-175-746-345/c

Sequence 345, Application US/10175746 Publication No. US20030027270A1 GENERAL INFORMATION:

APPLICANT:

Baker, Kevin P. Beresini, Maureen DeForge, Laura

APPLICANT:

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 ρ
 Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550 ; SEQ ID NO 345 ; LENGTH: 2933 ; TYPE: DNA ORGANIZM: Homo Sapien US-10-140-470-345
 US-10-123-904-345
RESULT 14
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 US-10-140-470-345/c
 Matches
 Query Match
Best Local :
 GENERAL INFORMATION:
 Publication No.
 Matches
 Query Match
Best Local Similarity
 CURRENT APPLICATION NUMBER: US/10/140,470 CURRENT FILING DATE: 2002-05-06
 APPLICANT: Zhang, Zemin
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FILE REFERENCE: P3330R1C160
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 APPLICANT:
 APPLICANT: Baker, Kevin P.
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 APPLICANT:
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Wood, William
 Gurney, Austin L. Sherwood, Steven
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 Gao, Wei-Qiang
 DeForge, Laura
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 Desnoyers, Luc
 Beresini, Maureen
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 38;
 38;
 Length 2933;
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 Indels
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 Gaps
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 0
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Filvaroff,Ellen

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SEQ ID NO 345
LENGTH: 2933
TYPE: DNA
ORGANISM: Homo Sapien
US-10-176-918-345
 RESULT 15
US-10-176-918-345/c
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 80
 Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 550
SEQ ID NO 345
LENGTH: 2933
TYPE: DNA
ORGANISM: Homo Sapien
US-10-175-746-345
 Sequence 345, Application US/10176918 Publication No. US20030027275A1
 APPLICANT: Zhang, Zemin
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FILE REFERENCE: P3330R1C382
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 GENERAL
 Query Match 12.1%;
Best Local Similarity 63.5%;
Matches 66; Conservative
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 APPLICANT:
 APPLICANT: Baker, Kevin P.
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 APPLICANT: Zhang, Zemin TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3330RIC353 CURRENT FILING DATE: 2002-06-19 CURRENT FILING DATE: 2002-06-19
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 2865 AAATTTATTTTGGAAAAATATTTTAAAAAGGAATTTCTTCATTA 2822
 80 TATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTA 123
 INFORMATION:
 Tumas, Daniel
Watanabe, Colin K
Wood, William
 Stewart, Timothy A.
 Sherwood, Steven
Smith, Victoria
 Godowski, Paul J. Gurney, Austin L.
 Goddard, Audrey
 Gerritsen, Mary E.
 Gao, Wei-Qiang
 Filvaroff, Ellen
 DeForge, Laura
 Beresini, Maureen
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Stewart, Timothy A. Tumas, Daniel Watanabe, Colin K
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Pred. No. 10;
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 38;
 or Palm
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 Gaps
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Search completed: March 30, 2003, 13:11:06 Job time : 31.2667 secs
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 Matches
 Query Match
Best Local Similarity
 2865 AAATTTATTTTGGAAAAATATTTTAAAAAGGAATTTCTTCATTA 2822
 80 TATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTA 123
 Conservative
 12.1%;
 Score 43.2; DB 9;
Pred. No. 10;
 Mismatches
 38;
 Length 2933;
 Indels
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 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 Minimum DB
Maximum DB
 Total number of hits satisfying chosen parameters:
 Title:
Perfect score:
 Scoring table:
 Run on:
 OM nucleic - nucleic search, using sw model
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 Query
Match
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10:
11:
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13:
14:
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 US-09-502-426A-1_COPY_6111_6468
 March 29,
 aaaaaaaaaagatgaaagt.....tgtcaaataccaaacacaag 358
 GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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194
423
1101
928
905
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12411.569 Million cell updates/sec
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 AL762543
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AL762544 Arabidops
AV787618 AV787618
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AL071865 Drosophil
AL077798 Drosophil
 Description
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AL41125/ T/ end of BH148938 ENTPT52TF	AQ880113 HS_4868_B	AL098462 Drosophil	AL107697 Drosophil	AL514657 AL514657	AL106171 Drosophil	ALZ29845 Tetraodon	ALZ3/857 Tetraodon	AL404635 T7 end of	ALU57169 Drosophil	AL514085 AL514085	AG043196 Pan trogl	AL425064 clone BA0	AL427102 clone BA0	ALIUI513 Drosophil	ALIU3735 Drosophil	AL106578 Drosophil	AL561361 AL561361	ALIU7122 Drosophil	ALU69706 Drosophil	ALU99876 Drosophil	ALU/5520 Drosophil	ALIU6197 Drosophil	AL108927 Drosophil	ALU65967 Drosophil	AL060732 Drosophil	AL419462 T3 end of	AL175696 Tetraodon	AL055924 Drosophil						ALU69257 Drosophil	_	ALIU6896 Drosophil	٠-		

## ALIGNMENTS

SOURCE ORGANISM DEFINITION Li,Y., Strizhov,N., Rosso,M. and Weisshaar,B.
Direct Submission
Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H. and Welsshaar,B.

A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines thale cress.
Arabidopsis thaliana
Arabidopsis, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; care eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. ROSSO,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics Unpublished AL762543 AL762543.1 GI:21508636 Unpublished GSS. AT762543 176 bp DNA linear GSS 19-JUN-2002 Arabidopsis thaliana T-DNA flanking sequence GK-025G03-013722, genomic survey sequence. (bases 1 to 176)

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TITLE
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 Submitted (17-JUN-2002) Weisshaar
 Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 AL762544
AL762544.1 GI:21508641
 Arabidopsis thaliana T-DNA flanking sequence GK-025G03-013757, genomic survey sequence.
 Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone T3A5. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line
 Direct Submission
 Unpublished
 and Weisshaar, B
 Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H
 Arabidopsis thaliana
 Unpublished
 A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA
 thale cress.
 http://www.mpiz-koeln.mpg.de/GABI-Kat/
 availability can be found at:
 transformed
 (bases 1 to 194)
 Conservative
 60
 Strizhov, N., Rosso, M.
 œ
 removed"
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pac106. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thalaina nuclear genome sequence were
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 27
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 Mismatches
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 and Weisshaar, B.
 56
B., Max-Planck-Institut fuer
 DNA
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 17;
 Indels
 linear
 Length 176;
 GSS 19-JUN-2002
 0
 Gaps
 0;
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 ATTGTCAAATACCAAACACAAG
 140;
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). This clone is in a
 RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074,
Tel: 81-298-36-4359
Fax: 81-298-36-9060
 Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
 Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone T3A5. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
 Unpublished (2002)
Contact: Motoaki Seki
 mRNA sequence.
AV787618
 AV787618 RAFL6 Arabidopsis thaliana
 Plant Functional Genomics Research Group
 Large scale analysis of Arabidopsis full-length cDNA (2002b)
 AV787618.1 GI:19806408
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 (bases
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/note="PCR was performed on DNA from Arabidopsis thaliana
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were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thalaina nuclear genome sequence were
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37 c 28 g 63 t
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 organism-"Arabidopsis thaliana"
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 2.1e-10;
 mRNA
 В
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 Length
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 EST 28-MAR-2002
 1;
 Gaps
 German
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FEATURES

modified web site further d

details

Location/Qualifiers

/clone\_lib="RAFL6"

source

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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information melanogaster genome using these BACs. For further information melanogaster BAC library was prepared by Kazutoyo Osoegawa and Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, EcoRI digestion of Drosophila and WX. The library is named RPCI-98 and was constructed by partial isogenic strain y2; cn bw sp, the same strain used for the BDGP from the P1 and EST libraries. A more detailed description of the library filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
 Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
 Submitted (11-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR48P19 of RPCI-98 library from Drosophila melanogaster (fruit
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/lab_host="DH10B"
/note="Site_1: SSII; Site_2: XhoI; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, hr) treatments"

79 c 64 g 124 t
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Pred. No. 1.8e-09;
 Mismatches
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 Length 423;
 Indels
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 Gaps
 from
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VERSION
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 SOURCE
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 JOURNAL
 ORIGIN
 ORGANISM
 BASE COUNT
 Matches
 Query Match
 source
 - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila please see http://www.fruitfly.org The BDGP See T
 244 AAACCTTAAATGGGCTTT 261
 843
 783
 184
 723 KKATKTKKKDKKAAWAAADKKDRKKGGKKGKKGKKGKKGGKKKKKKKKKGKGGWGKKGKKK
 663
 124 GTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAG 183
 64 TITITGCCCAATGATATATAAAATTTGGATAAATATATTATTGGATATTCGTTTTTTA 123
 Local
 TKDKGKKKKKTKKKTTKK 860
 AGDDDAKDKTKKKKKAATTTTKKKKGKKKKKKAAKKKKAADRTKKTKWDAAAAAAAKK 842
 CTAGGTTGAGTCTTTGGACATTTGTATTGGATGTTGTTGATTAGTGTCGACACTATT
 TTTTTTTTTTATTAAATAAAAAWTTTDTWAAAWWTTTKKKKKKAAAADKWKDAKKWDGA
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
 Genoscope.
 GSS
 Drosophila melanogaster genome sur
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 Similarity
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 genomic survey sequence.
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 19.0%;
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 Score 68; I
 928 bp
 Mismatches
 survey sequence T7 end of BAC #
 151 t
 Drosophila melanogaster
 DB 17;
 DNA
 90;
 406 others
 Length 1101;
 linear
 Indels
 0;
 Gaps
 782
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FEATURES

source

REFERENCE AUTHORS

JOURNAL TITLE

Genoscope.
Direct Submission

ACCESSION VERSION

KEYWORDS

AL078714.1 GI:5102004 GSS.

survey sequence.

ORGANISM

RESULT 4 CNSOOLT2

DEFINITION POCAS

CNSOOLT2

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121 T 121

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BASE COUNT

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Matches 121; Query Match

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33.8%; 50 100.0%; Pr

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Web : www.genoscope.cns.fr)

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Matches 99
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 584
 824
 644
 524
 301
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 241
 704
 181
 121
 61
 Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila baA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
 TTAGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGG
 TTTTTTTGCCCAATGATATATAAAAATTTGGATAAATAATAATTATTGGATATTCGTTTT 120
 KAAKKKKKKKKKKKKKK 842
 ATTAAACCTTAAATGGGCTTTCTATAAGGCCCCAATTATATTACGATTATAACAAAGTGAC
 TTAWTTTTTTTTTTTTTTATWAWATAWAAATATWAWAWATWTWDGKNWNNNAWW
 GAGCTAGGTTGAGTCTTTGGACATTTGTATTGGATGTTGATTATTAGTGTCGACACT
 WTAWTWTTATATAWAAAWAAAAWAAAAAWAATAAAAAATTTTAWAAWTAAAAWAAAAAT 703
 AAAAWAATWITTITWWITITWAWAAAWIAITITWITITITTITTITWAWIITTAAITWI 583
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 fly), genomic survey sequence. AL077798 AL077798.1 GI:4957174
 CNSOOKHX 905 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC: BACR17N06 of RPCI-98 library from Drosophila melanogaster (fruit
 Genoscope.
 Direct Submission
 Drosophila
 Drosophila melanogaster.
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 (bases 1 to 905)
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31.0%;
 83;
 T7"
 Score 65.4;
Pred. No. 0.
 Mismatches
 905 bp
 g
 melanogaster"
 321 t
 DB
. 27;
 137;
 17;
 191 others
 Indels
 Length
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 Gaps
 180
 643
 763
 240
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 Matches
 Query Match
 301
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 702
 Local
 388
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582 AHAAWAMWWATMTTWTMTWATAATTTTMAMHMAAWWAWYYMMMMCWAACA
 121 TTAGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGG
 822 WITTIWIWIATIWWIATAAWIATWDIAWIATAWIWIAATITIIWATAIATWIAICWYIW
 61 TTTTTTTTGCCCAATGATATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTT 120
 ATTAAACCTTAAATGGGCTTTCTATAAGGCCCAATTATATTACGATTATAACAAAGTGAC
 AACTTTTACTTCGTTTTTGATCCGAAGCAATAACAAATTGTCAAATACCAAACA 354
 TTTTTTTTTTTATTTTTTTTTTTTATWTATTATWATTTATWTTDTTTTTTMWTAWWWWM
 GAGCTAGGTTGAGTCTTTGGACATTTGTATTGGATGTTGTTGATTATTAGTGTCGACACT
This sequence is a single read and was generated as part of a lascale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
 2 (bases 1 to 1027)
Roest-Crollius,H., Jaillon,O.,
Bouneau,L., Billault,A., Quetie
Weissenbach,J.
 Tetraodontidae; Tetraodon.

1 (bases 1 to 1027)

Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottler,P., Quetler,F.,
Saurin,W. and Weissenbach,J.
 GSS; genome survey sequence. Tetraodon nigroviridis. Tetraodon nigroviridis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthopterygii; Percomorpha; Tetraodontiformes;
 CNS02T50 1027 bp DNA linear GSS 1 Tetraodon nigroviridis genome survey sequence T7 end of c 163Ml6 of library G from Tetraodon nigroviridis, genomic
 Submitted (12-APR-2000)
 Human gene number estimate
Tetraodon nigroviridis DNA
 Unpublished
 Charaterization and
 Unpublished
 AL212733.1 GI:7871552
 freshwater pufferfish
 Similarity
 (bases 1 to 1027)
 Conservative
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 þ
 /clone_lib="RPCI-98"
/note="end : T7"
82 c 77 g
 35.9%;
 repeat analysis of the compact genome of the sh Tetraodon nigroviridis
 59;
 Score 60; Pred. No. 1
 On,O., Dasilva,C., Fizames,C., Fisher,C., Quetier,F., Saurin,W., Bernot,A. and
 Mismatches
 provided sequence
 194
 r
 ЬĀ
 168;
 genome
 164
 Length 905
 Indels
 others
 wide
 analysis using
 GSS 15-MAY-2000
of clone
 529
 0;
 Gaps
 survey
 180
 240
 763
 643
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Location/Qualifiers

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 Query Match
 BASE COUNT
 JOURNAL
 TITLE
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 Matches
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Best Local :
 737
 source
61 TTTTTTTTGCCCAATGATATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTT 120
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 647
 121 TTAGTTCGGGTTTGAGAAAA 140
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 WAWAAAAATTKATDTTTTTTTTTTWTTTWTTTTTBTTTTATWTTTTAKDTTTTTTTW 796
 TTATTTATWAATTTANAAAA 568
 TTTTTTTGCCCAATGATATAAAAATTTGGATAAATAATAATATTATTGGATATTCGTTTT 120
 Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centred European the Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
 Similarity
 Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
 Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
 Genoscope.
 Direct Submission
 CNS016LI 1101 bp DNA linear GSS 26-JUL-19 Drosophila melanogaster genome survey sequence T7 end of BAC BACN16D22 of DrosBAC library from Drosophila melanogaster (fruit
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34.3%; Pred. No. 3
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 21;
 84 g
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 Mismatches 156;
 Mismatches
 158 t
 DB 17; Length 1101;
 DB 17;
 47;
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 Indels
 Indels
 Length 1027;
 2;
 GSS 26-JUL-1999
 0,
 Gaps
 Gaps
 648
 T7"
 1;
 0
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RESULT 9
AZ691838/c
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Best Local Similarity
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 1035
 301 AACTTTTACTTCGTTTTTGATCCGAAGCAATAACAAATTGTCAAATACCAAACACA 356
 975
 241 ATTAAACCTTAAATGGGCTTTCTATAAGGCCCAATTATATTACGATTATAACAAAGTGAC 300
 915 WAWWAWAATTATWTWATTATDWRTTTASTATWTTTDTWTWATAWRAKAWRWATWDWAW 974
 855
 121
 797
 AATWTWTTKWTTKWKTTTKWTTTKTAKTKAKAGRAWWWWRTKAARRWWRWTRTADA 1090
 AWRATANDTATWAATADATTWATATAAANWTWWDTATTGWRWAWTADATTANDAAATRTA 1034
 AWTATAWWATAWTWWWWTRTAWWWTDWTWWWWATTAKTTWATWATATTAWTWAWAWWTA 914
 TTAGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGG 180
 High quality sequence start: 48
High quality sequence stop: 291
Location/Qualiflers
 Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the
 Class: shotgun
 Seq primer: M13-Forward
 DNA library
 Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
 HM1: IMSS sheared DNA library
 Loftus, B., Van Aken, S. and Fraser, C. Determination of clone end sequences
 AZ691838 961 bp DNA linear GSS 14-DEC-200 ENTMISOTF Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, DNA sequence.
 Contact: Brendan J Loftus
 Eukaryota; Entamoebidae;
 Entamoeba histolytica
 Entamoeba histolytica.
 AZ691838.1 GI:11828984
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 (bases 1 to 961)
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Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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DB 17;
1.8;
 MD 20850,
 from Entamoeba histolytica
 histolytica HM1:IMSS sheared
 USA
 GSS 14-DEC-2000
 854
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Length 961;

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VERSION

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RESULT 10
CNS00EJ4/c
 REFERENCE
AUTHORS
TITLE
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 FEATURES
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ORGANISM
 DEFINITION
 KEYWORDS
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 Matches 149;
 Matches
 JOURNAL
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 835
 895
 121 TTAGTTCGGGTTT-----
 121
 614
 674
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 Local Similarity
 61
 BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPC1-98 and was constructed by partial EcoRI digestion of Drosophila BNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library or
 _
 TWATTTWTAADADAAAAAWDAAAAAGGAAAAAAAAWGAATTTTTTTGGTAAAAAWAWA
 TTTTTTTTGCCCCAATGATATAAAAATTTGGATAAATAATAATTATTGGATATTCGTTTT 120
 TTAGTTCGGGTTT 133
 TTTTTTTTGCCCCAATGATATAAAAATTTTGGATAATAATAATATTGGATATTCGTTTT 120
 TTTTTTTTTTTT 542
 Drosophila melanogaster genome survey sequence T7 end of EBACR29K22 of RPCI-98 library from Drosophila melanogaster
 and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 Drosophila melanogaster
 Direct Submission
 Genoscope
 Drosophila melanogaster.
 AL069257.1
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AL069257
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 35,
 0;
 Score 57; DB Pred. No. 4.6;
 25 g
 Mismatches
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 Mismatches
 ģ
 p DNA linear GSS 04-JU
survey sequence T7 end of BAC
 377 t
 DB 17;
 163;
 47;
 125 others
 Length 1101;
 Indels
 Indels
 GSS 04-JUN-1999
 7;
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 Gaps
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 164
 595
 200
 140
 224
 775
 284 TTTTTTTTTTTTTTTTTTTTTTTTTKKTTTTBTKYKGTTTTKTTTGTWKTTTYYT 225
 294 AAGTGACAACTTTTACTTCGTTTTTGATCCGAAGCAATAACAAATTGTCAAATA 347
 174
 80 TATAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTAGTTCGGGTTTGAGAAA 139
 Local
ACCTWAYCCWKTTGCCAAKKTGKTWTWTTTTTTTTKTTKKTTWTTTKKTTTAGGGKTTAT 105
 TTWTKATWWAKTKAYGTWTTTTKKTTWKTWTWWTTATTTKWCTKWTTTWTKTWTGWTWTK 165
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 TIWITAATGDGKTTTTTGGGGAGWTAAGGGGTWATTTTTTATAGRYTATTTTAATTTTT 716
 AGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTAGGTTGAGTCTTTG 199
 CGACACTATTAAACCTTAAATGGGCTTTCTATAAGGCCCAATTATATTACGATTATAACA 293
 101;
 - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
 Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
 Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
 CNS018BG 894 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN13B16 of DrosBAC library from Drosophila melanogaster (fruit
 Similarity
 Direct Submission
 Genoscope
 Drosophila melanogaster
 AL109126.1 GI:5629430 GSS.
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 Score 56.6;
Pred. No. 6;
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 Mismatches
 138
 4
 DB 17;
 118;
 118 others
 Length 894;
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of a

COMMENT

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ORIGIN

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Gaps

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 BASE COUNT
ORIGIN
 PUBMED
REFERENCE
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 PUBMED
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 COMMENT
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KEYWORDS
 RESULT 12
CNS073CX
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 80
 Matches
 REFERENCE
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 ACCESSION
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 AUTHORS
TITLE
 MEDLINE
 JOURNAL
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 ORGANISM
 AUTHORS
 source
AL Submitted (08-5EP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zyoosaccharomyces rouxii, Saccharomyces kluyverori, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Sh were prepared and both extremities were sequenced. See the vocation of this sequence and for the sequence of the other extremity of this insert.
 104
 44
 TTTWKWWCTTKWTWTTTTKKTTWTTTTTTTTTAGTTTAATATTTTTATTATATATATATTAT 45
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 Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J., Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
FBBS Lett. 487 (1), 3-12 (2000)
 Similarity
 Direct Submission
 Bolotin-Fukuhara,M., Toffano-Nioche,C., Artiguenave,F., Duchateau-Nguyen,G., Lemaire,M., Marmeisse,R., Montrocher,R., Robert,C., Termiter,M., Wincker,P. and Wesolowski-Louvel,M. Genomic exploration of the hemiascomycetous yeasts: 11.
 Kluyveromyces lactis
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.

1 (bases 1 to 1147)
 Kluyveromyces lactis
 FEBS
 CNS073CX 1147 bp DNA linear clone BA0AB018F06 of library BA0AB from strain CLIB
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 Kluyveromyces lactis, genomic survey sequence.
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 (bases 1 to 1147)
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 Lett. 487 (1), 66-70 (2000)
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Pred. No. 5.1;
99; Mismatches
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 98;
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 122 TAGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGA 176
 952 TTTTTGMATTWWWTTTKNTDAGTAAWWAATTTTTWATAATTTTTTKRTTTTTTTTTTTT
 source
 892 WAAAAAAAAAAWAAAAAWIITWIITITTWIAAITWWITTITTTWATTTTAAAWAAAAA
 62
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 190
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 745
 685 AANTTTAAATTTTTNAATATNTTTTTTTTTTTTTTTGNATATWAWAAAAAAAAWTWTTTTT
 TTTTTTTGCCCAATGATATATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTT
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 GTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTAGGT 189
 Submitted (23-ULI-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
 Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)
 Similarity
 fly), genomic AL097397
 CNS0029N 1101 bp DNA linear GSS 26-JUL-1999 Drosophila melanogaster genome survey sequence T7 end of BAC BACK01C10 of DrosBAC library from Drosophila melanogaster (fruit
 Direct Submission
 Drosophila melanogaster.
 AL097397.1 GI:5609008
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288 c 267 g
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Pred. No. 5
 Mismatches
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 BB
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 17;
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 115 others
 Length 1101;
 Indels
 0;
 Gaps
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 573
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 300 CAACTTTTACTTCGTTTTTGATCCGAAGCAATAACAAATTGTCAAATACCAAA 352
 240
 181
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 121
 61
 Local Similarity
 Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a bollaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers
 GAGCTAGGTTGAGTCTTTGGACATTTGTAT-TGGATGTTGTTGATTAGTGTCGACAC
 TATTAAACCTTAAATGGGCTTTCTATAAGGCCCAATTATATTACGATTATAACAAAGTGA
 AAAATTAAAATTAAWAAAAAAAAAAAAAAAAAWTAATTAAWAAAAAWTAA
 TTAGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGG
 TTTTTTTTGCCCAATGATATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTT 120
 Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 CNS0021J 1101 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC #BACR05N11 of RPCI-98 library from Drosophila melanogaster (fruit
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 Genoscope.
 Drosophila melanogaster.
 AL061936.1 GI:4940214
 fly), genomic survey sequence. AL061936
 Direct Submission
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 Conservative
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Pred. No. 6.
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 DB 17;
 H
 171;
 146
 Indels
 Length 1101;
 others
 1;
 Gaps
 634
 180
 239
 574
 1;
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RESULT 15

Search completed: March 30, Job time: 474.144 secs

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 700
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 124 GTTCGGGTTTGAGAAAAGGGTTTCGACTTT 153
 64
 TTTTTTTTTTAAAAWTTTTTTAWWTTT
 TTTTTGCCCAATGATATATAAAATTTGGATAATAATATTATTGGATATTCGTTTTTTA 123
 GSS; genome survey sequence. Tetraodon nigroviridis. Tetraodon nigroviridis
 This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cng.fr/Tetraodon.
 CNSO4AIH

949 bp DNA linear GSS 21-MAY-:
Tetraodon nigroviridis genome survey sequence T7 end of clone
095F19 of library G from Tetraodon nigroviridis, genomic survey
 Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
 Tetraodontidae; Tetraodon.

1 (bases 1 to 949)
Roest-Crollius, H., Jaillon, O., Dasilva, C.,
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 Submitted (12-APR-2000)
 Unpublished
 Weissenbach,
 Bouneau, L., Billault, A.,
 2 (bases 1 to 949)
Roest-Crollius, H.,
 Unpublished
 Human gene number estimate
 Saurin, W. and Weissenbach, J.
 Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetie
 Direct Submission
 Genoscope.
 Tetraodon nigroviridis DNA
 Similarity
 (bases 1 to 949)
 355
 Conservative
 /clone_11b="G"
/note="Genoscope sequence ID : C0BG095CC10LP1-end : T7"
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/clone="095F19"
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 Jaillon, O.,
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 Score 56;
Pred. No. 7
 Mismatches
 on,O., Dasilva,C., Fizar
Quetier,F., Saurin,W.,
 provided by genome wide analysis using sequence
 DB 17;
 55;
 Length 949
 Fizames, C.,
 Indels
 Bernot, A.
 eau,L., Fisher,C.
Quetier,F.,
 part of a large nigroviridis
 GSS 21-MAY-2000
d of clone
 0,
 Fisher, C.
 Gaps
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 0
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